

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 06:34:51 ; Search time 40 Seconds
(without alignments)
584.517 Million cell updates/sec

Title: US-10-662-431-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNELKQMCKYKSGIACFL.....NEHLIDMDHEASFFGAFVLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 125689

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	134.5	10.5	204	1	S17289	tumor necrosis fac
2	131.5	10.2	234	1	A25451	tumor necrosis fac
3	130	10.1	232	1	S12606	tumor necrosis fac
4	129.5	10.1	235	2	I54490	tumor necrosis fac
5	127.5	9.9	204	1	S24641	lymphotoxin - bovi
6	126	9.8	234	1	JQ1344	tumor necrosis fac
7	123	9.6	233	1	QWHUN	tumor necrosis fac
8	122	9.5	205	1	QWHUX	lymphotoxin alpha
9	121	9.4	235	1	QWMSN	tumor necrosis fac
10	121	9.4	235	2	JU0029	tumor necrosis fac
11	120	9.3	233	1	S22052	tumor necrosis fac
12	117.5	9.1	234	1	JH0529	tumor necrosis fac
13	115.5	9.0	193	2	S06192	tumor necrosis fac
14	114	8.9	202	1	B27303	tumor necrosis fac
15	113.5	8.8	185	2	S52715	tumor necrosis fac
16	113	8.8	233	1	S24642	tumor necrosis fac
17	111.5	8.7	202	1	JN0869	tumor necrosis fac
18	107	8.3	197	1	JH0309	tumor necrosis fac
19	98.5	7.7	233	2	S11688	tumor necrosis fac
20	80.5	6.3	203	2	C89803	hypothetical prote
21	78	6.1	202	2	A82076	conserved hypothet
22	77	6.0	223	2	H71485	hypothetical prote
23	76.5	5.9	195	2	S77753	peptide transport
24	75.5	5.9	142	2	B87569	dnak suppressor pr
25	74	5.7	201	2	E82910	hypothetical prote
26	73	5.7	223	2	B64396	hypothetical prote
27	73	5.7	227	2	B70438	hypothetical prote
28	72.5	5.6	112	2	AF0347	conserved hypothet
29	72.5	5.6	123	2	T26862	hypothetical prote

30	72.5	5.6	156	2	H71623	probable secreted
31	72.5	5.6	218	2	A99014	hypothetical prote
32	72.5	5.6	243	2	A99387	sAM-dependent meth
33	71.5	5.6	195	1	I40422	conserved hypothet
34	71.5	5.6	227	2	H64336	formate dehydrogen
35	71	5.5	234	2	T21543	hypothetical prote
36	70.5	5.5	189	2	D45188	chitin synthase (E
37	70.5	5.5	222	2	T37839	hypothetical prote
38	70.5	5.5	226	2	C81749	conserved hypothet
39	70	5.4	209	2	D90593	lipoprotein [impor
40	69.5	5.4	144	2	H81292	hypothetical prote
41	69.5	5.4	199	2	JE0351	OX40 ligand protei
42	69.5	5.4	201	2	S53800	chitin synthase (E
43	69.5	5.4	202	2	B90180	ABC transporter, A
44	69.5	5.4	222	2	A81896	hypothetical prote
45	69	5.4	139	2	T28300	ORF MSV139 hypothe

ALIGNMENTS

RESULT 1

S17289
tumor necrosis factor beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S17289
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative analy
A;Reference number: S17289; MUID:91340150; PMID:1874444
A;Accession: S17289
A;Molecule type: DNA
A;Residues: 1-204 <KUH>
A;Cross-references: UNIPROT:P26445; EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133
C;Genetics:
A;Introns: 32/3; 68/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match	10.5%;	Score 134.5;	DB 1;	Length 204;
Best Local Similarity	24.7%;	Pred. No. 0.00039;		
Matches	46;	Conservative	31;	Mismatches 76; Indels 33; Gaps 7;
QY	63	STVQEKQNI SPLVRERGPORVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS	115	
Db	42	SAAQPAHQH-PPKHLARGTLKPAHLVGDPTDPSLRWRANT-----DRAFLR----	88	
QY	116	WESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY	175	
Db	89	-----HGFL-----LSNNSLLVPTSGLYFVYSQVWFSGEGCFPKATPTPLYLAHEVQLF	137	
QY	176	TS-YPDPILLMKSAARNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEA	234	
Db	138	SSQYPFHVPLLSAQKSVCPGQGPW-VRSVYQGA VFLLTQGDQLSTHTDGTPHLLSPSS	196	
QY	235	SFFGAF 240		
Db	197	VFFGAF 202		

RESULT 2

A25451
tumor necrosis factor alpha precursor - rabbit
N;Alternate names: cachectin; TNF alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A25454; A25451; JS0727
R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.;
DNA 5, 149-156, 1986
A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabt

RESULT 6
JQ1344
tumor necrosis factor alpha precursor - horse
N;Alternate names: cachectin; TNF alpha
C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JQ1344
R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A;A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
A;Reference number: JQ1344; MUID:92084125; PMID:1748301
A;Accession: JQ1344
A;Molecule type: DNA
A;Residues: 1-234 <SUX>
A;Cross-references: UNIPROT:P29553; GB:M64087; NID:q164244; PIDN:AAA30959.1; PID:q164245

Lymphokine Res. 7, 175-185, 1988

A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and

A;Reference number: A61478; MUID:88301617; PMID:2841543

A;Accession: A61478

A;Molecule type: protein

A;Residues: 56-79;86-95,'X',97,'X',99;119-151,'XX',154-162,'X',164,'X',166,'X',168,'X',1

R;Voigt, C.G.; Maurer-Fogy, I.; Adolf, G.R.

FEBS Lett. 314, 85-88, 1992

A;Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylation

A;Reference number: S26951; MUID:93083656; PMID:1451807

A;Accession: S26951

A;Molecule type: protein

A;Residues: 35-59,'N',61-205 <VOI>

A;Note: 60-Thr was also found

R;Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.

Arch. Biochem. Biophys. 304, 144-153, 1993

A;Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO

A;Reference number: S34742; MUID:93311995; PMID:8323280

A;Contents: annotation

C;Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction, while having no detrimental effect on normal cells. It can also act synergistically with

C;Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of different activities but are produced by different cell types and have different induction kinetics

C;Genetics:

A;Gene: GDB:LTA; LT; TNFB

A;Cross-references: GDB:120442; OMIM:153440

A;Map position: 6p21.3-6p21.3

A;Introns: 33/3; 69/1

A;Note: the first intron occurs before the initiator codon

C;Superfamily: tumor necrosis factor

C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage

F;1-34/Domain: signal sequence #status predicted <SIG>

F;35-205/Product: lymphotoxin #status predicted <MAT>

F;41/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental

F;96/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 9.5%; Score 122; DB 1; Length 205;

Best Local Similarity 23.4%; Pred. No. 0.0046;

Matches 37; Conservative 29; Mismatches 72; Indels 20; Gaps 5;

Qy 85 AAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRGHSFLSNLHLRNGELVIHEKGFY 144

Db 64 AAHLIGDPKQNSL-----LWRANTDRAFLQDGFSLSNSLLVPTSGIY 107

Qy 145 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS-YDPDILLMKARSNCWSKDAEYGLYS 203

Db 108 FVYSQVVFSGKAYSPKATSSPLYLAHEVQLFSSQYFFHVPLL-SSQKMVYPGLQEPWLHS 166

Qy 204 IYQGGIFELKENDRIFVSVTN-EHLIDMDHEASFFGAF 240

Db 167 MYHGAFAQLTQGDLSTHTDGIPHLV-LSPSTVFFGAF 203

RESULT 9

QWMSN

tumor necrosis factor alpha precursor - mouse

N;Alternate names: cachectin; TNF alpha

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 09-Jul-2004

C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696

R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.

DNA 7, 193-201, 1988

A;Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis

A;Reference number: A22908; MUID:88224564; PMID:2836146

A;Accession: A22908

A;Molecule type: DNA

A;Residues: 1-235 <SHI>

A;Cross-references: UNIPROT:P06804; GB:M20155

R;Shakhov, A.N.; Nedospasov, S.A.

Bioorg. Khim. 13, 701-705, 1987

A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucle

A;Reference number: S03791; MUID:87298639; PMID:3040015

A;Accession: S03791

A;Molecule type: DNA

A;Residues: 1-235 <SHA>

A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087

A;Note: article in Russian with English abstract

R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.

Nucleic Acids Res. 15, 9083-9084, 1987

A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor necr

A;Reference number: A93679; MUID:88067722; PMID:3684584

A;Accession: A27303

A;Molecule type: DNA

A;Residues: 1-235 <SEM>

A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832

R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.

Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985

A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis

A;Reference number: A25164; MUID:85298296; PMID:3898078

A;Accession: A25164

A;Molecule type: mRNA

A;Residues: 1-235 <PEN>

A;Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085

R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, I

Nucleic Acids Res. 13, 4417-4429, 1985

A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expres

A;Reference number: A23127; MUID:85242112; PMID:2989794

A;Accession: A23127

A;Molecule type: mRNA

A;Residues: 1-235 <FRA>

A;Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845

R;Cseh, K.; Beutler, B.

J. Biol. Chem. 264, 16256-16260, 1989

A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results i

A;Reference number: A34251; MUID:89380231; PMID:2777790

A;Accession: A34251

A;Molecule type: protein

A;Residues: 70-87 <CSE>

R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.

Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986

A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region of

A;Reference number: I59058; MUID:86149365; PMID:2419912

A;Accession: I59058

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-230,'R',232-235 <RES>

A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083

R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.

Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990

A;Title: Characterization of high molecular weight glycosylated forms of murine tumor nec

A;Reference number: A36696; MUID:91097531; PMID:2268312

A;Accession: A36696

A;Molecule type: protein

A;Residues: 80-85,'X',87-99 <SHE>

C;Genetics:

A;Introns: 62/3; 81/1; 97/1

A;Note: the first intron occurs in the 5'-untranslated region

C;Superfamily: tumor necrosis factor

C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membr

F;80-235/Product: tumor necrosis factor #status experimental <MAT>

F;20/Binding site: myristate (Lys) (covalent) #status predicted

F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;148-179/Disulfide bonds: #status predicted

Query Match 9.4%; Score 121; DB 1; Length 235;

Best Local Similarity 23.1%; Pred. No. 0.0066;

Matches 43; Conservative 34; Mismatches 79; Indels 30; Gaps 8;

Qy 67 EKQQNISPLVRERGPPQVAAHITGTRGRSNTLSSP-----NSKNEKALGRKINSWESSR 120

Db 62 EXFPNGPLI-----SSMAQTLTLRSSSQNSDDKPAHVAVANHQVEQL-----EWLSQR 111

Qy 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYP 179

Db 112 ANALLANGMDLKDNLVVPADGLYLVYSQVLFGKQ-----GCPDYVLLTHTVSRFAISYQ 166


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Qy 180 DPILLMKSARNSCWSKDAEYG-----LYSIYQGIGIFELKENDRIFVSVTNEHLIDMDHE 233
Db 167 EKVNLLSAVKSPC-PKDTPEGAELKPWYEPYILGGVVFQLEKGDQLSAEVLNPKYLDFAES 225

Qy 234 AS-FFG 238
Db 226 GQVYFG 231

RESULT 10
JU0029
tumor necrosis factor alpha precursor - rat
N:Alternate names: cachectin; TNF alpha
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: JU0029; JN0868; S21674
R:Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A:Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis f
A:Reference number: JU0029
A:Accession: JU0029
A:Molecule type: DNA
A:Residues: 1-235 <SHI>
A:Cross-references: UNIPROT:P16599
R:Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A:Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
A:Reference number: JN0868; MUID:94040766; PMID:8224868
A:Accession: JN0868
A:Molecule type: DNA
A:Residues: 1-235 <KWO>
A:Cross-references: GB:I00981; NID:G205253; PIDN:AAA16275.1; PID:G205254
R:Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A:Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitr
A:Reference number: S21674; MUID:92329007; PMID:1627266
A:Accession: S21674
A:Molecule type: mRNA
A:Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 <EST>
A:Cross-references: GB:X66539; GB:S40199; NID:G395369; PIDN:CAA47146.1; PID:G395370
C:Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and
C:Genetics:
A:Gene: TNF-alpha
A:Introns: 62/3; 81/1; 97/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F:80-235/Product: tumor necrosis factor #status predicted <MAT>
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:148-179/Disulfide bonds: #status predicted

Query Match          9.4%;   Score 121;   DB 2;   Length 235;
Best Local Similarity 23.0%;   Pred. No. 0.0066;
Matches 43;   Conservative 35;   Mismatches 79;   Indels 30;   Gaps 8;

Qy 66 QEQQNTSPLVRERGPQVAAHITGTRGRSNTLSSP-----NSKNEKALGRKINSWESS 119
Db 61 EEKFPNGUPLI-----SSMAQTTLRSSSQSSDDKPVAAHVVAHQAEQL-----EWLSQ 110

Qy 120 RSGHSFTLSNHLRNGELVIEHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SY 178
Db 111 RANALLANGMDLKDNLVVPADGLYLIYSQVLFKGQ-----GCPDYVLLTHTVSRFAISY 165

Qy 179 PDPILLMKSARNSCWSKDAEYG-----LYSIYQGIGIFELKENDRIFVSVTNEHLIDMDH 232
Db 166 QEKVSLLSAISKSPC-PKDTPEGAELKPWYEPMPYLVGGVVFQLEKGDLLSAEVLNPKYLDITE 224

Qy 233 EAS-FFG 238
Db 225 SGQVYFG 231

```


Search completed: June 3, 2005, 06:44:42
Job time : 42 secs

R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g1369902
R;Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Golan, J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 186; DB 2; Length 281;
Best Local Similarity 22.1%; Pred. No. 3.4e-08;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

Qy 4 MEVQGPSLGQTCVLIVIFTVLQSLCVAV---TYVYFTNELKQMDKYKSGIACFLKE 60
Db 71 LKKGNGHSTG-LCLLVMFVVLVALVGLGLGMFQLFHLQKELAEIRESTSQMHTASSLEK 129
Qy 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
Db 130 QIGHPSPPPE-----KKELRKV----- 146
Qy 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHERG 180
Db 147 ---AHLT---GKSNSRSM-----LEWEDT-YGIVLLSGVKYKGGGLVINETG 187
Qy 181 FYIYISQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYDPDPILLMKSARNS-----CWSK 233
Db 188 LYFVYSKVYFRGQ-----SCNNPLSLSHKVMRNSKYPQDLVNMEGKQMSYCTTGQMMAR 241
Qy 234 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Db 242 -----SSYLGAVFNLTADHLYVNVSELSLVNFEEESQTFFGLY 279

RESULT 3
A49266
fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor gene family.
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
A;Cross-references: UNIPROT:P36940; GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C;Keywords: glycoprotein; transmembrane protein

Query Match 12.0%; Score 177.5; DB 2; Length 278;
Best Local Similarity 27.5%; Pred. No. 1.8e-07;
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

Qy 100 ISTVQEKQONISPLVRERGPQVAAAHITGT-RGRSNTLSSPNKNEKALGRKINSWESSR 158
Db 121 VSSFEKQIANPSTPSETKKPRSV-AHLTGNPRSRSIPL-----EWEDT- 162
Qy 159 SGHSFLSNLHRLNGELVIHEKGFYIYISQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYP 217
Db 163 YGTALISGVKYKGGVLVINEAGLYFVYSKVYFRGQ-----SCNSQPLSHKVMRNFKYP 216
Qy 218 DPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
Db 217 GDLVLMEEKLNYCTT--GQIWAHSSYLGAVFNLTJADHLYVNIQSLSLINFEEESKTFEG 274
Qy 277 AF 278
Db 275 LY 276

RESULT 4
S53090
CD40 ligand - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S53090
R;Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
A;Accession: S53090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <MER>
A;Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g73257

Query Match 11.1%; Score 164; DB 2; Length 261;
Best Local Similarity 25.9%; Pred. No. 2.3e-06;
Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;

Qy 6 VQGPSLGQTCVLIVIFTVL--QSLCVAVTYVYFTNELKQMDKYKSGIACFLKEDDS 63
Db 13 VATGPPVSMK-IFMYLLTVFLITQWIGSALFAVYLHRRLDKIEDERNLHEDFVFMK---T 68
Qy 64 YWDPNDEESMNS--PCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPQ 121
Db 69 IQRCKGEGSLLLNCEEIRSFEDLV-KDIMQNK-----VKKKEKNFEMHKGDOEPQ- 121
Qy 122 VAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHE 178
Db 122 IAAHV-----ISEASKTTSVL-----QW--APKGYITLSNNLVTLENGKQLAVKR 165
Qy 179 KGFYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWSKDAEYG 238
Db 166 QGFYIYTQVTFCSNRE----TLSQAPFIASLCLKSPSGSERILLRAANTHSSSKPC--G 219
Qy 239 LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
Db 220 QQSIHLGGVFELQSGASVFVNVTDPQSVSHGTGFTSFG 257

RESULT 5
I53476
CD40 ligand - human
N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; EMBO J. 11, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for

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A;Reference number: S28017; MUID:93049181; PMID:1385114
A;Accession: S28017
A;Molecule type: mRNA
A;Residues: 1-261 <HOL>
A;Cross-references: UNIPROT:P29965; EMBL:Z15017; NID:g38483; PIDN:CAA78737.1; PID:g38484
R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
J. Exp. Med. 176, 1543-1550, 1992
A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin
A;Reference number: JH0793; MUID:93094757; PMID:1281209
A;Accession: JH0793
A;Molecule type: mRNA
A;Residues: 1-261 <SPR>
A;Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412
A;Experimental source: peripheral blood T-cell
R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek, R.A.
Eur. J. Immunol. 22, 3191-3194, 1992
A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A;Reference number: S26694; MUID:93076854; PMID:1280226
A;Accession: S26694
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <GRA>
A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270
R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
FEBS Lett. 315, 259-266, 1993
A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e
A;Reference number: S28852; MUID:93138085; PMID:7678552
A;Accession: S28852
A;Molecule type: mRNA
A;Residues: 1-261 <GAU>
A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
C;Genetics:
A;Gene: GDB:CD40LG; HIGM1; IMD3
A;Cross-references: GDB:120632; OMIM:308230
A;Map position: Xq26-Xq26
C;Keywords: glycoprotein; transmembrane protein
F;13-44/Domain: transmembrane #status predicted <TMM>
F;45-261/Domain: extracellular #status predicted <EXT>
F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          10.0%; Score 147.5; DB 2; Length 261;
Best Local Similarity 23.7%; Pred.No. 5.7e-05;
Matches 66; Conservative 51; Mismatches 99; Indels 63; Gaps 15;

QY      17 VLIIVFTVLL--QSLCAVTYYVFTNELKQMDDKYSGKIACFLKEDDSYWDP-----ND 69
Db       : : : | | | : | : | | : | : | : | : | : | : | : | : | : | : | : | :
Dbb      23 IFMYLLTVPLITQMIGSALFAVYLHRRRLDKIEDRN-----LHEDFVFMTIQR CNTG 75

QY      70 EESMN-SPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPQVAAHITG 128
Db       | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | :
Dbb      76 ERSLSLLNCEEIKSQFEGFKDIML-NKEET-----KKENSFEMQKGDNQPQ-IAAHV-- 126

QY      129 TRGRSNTLSSPNKNKALKGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHEKGFYYII 185
Db       : | : | : | | | | | | | | : | : | : | : | : | : | : | : | : | :
Dbb      127 -----ISEASSKTTSVL-----QW--AEKGYTMSNNLVLTLENGKQLTVKRQGLYYII 172

QY      186 SQTYFRFQEEIKEENT-----KNDKMQVQYIYKYTSYPDPILLMKSAARNCSWSKDAEY 237
Db       : | : | | | | | : | : : | : : : | : : : | : : : | : : : | : : : |
Dbb      173 AQVTFCSNRREASSQAFPIASCLCKSPGRPER-----ILLRAANTHSSAKPC-- 218

QY      238 GLYSIQGGIFELKENDRI FVSVTNEHLIDMDHEASFFG 276
Db       | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | :
Dbb      219 GQSIHLGGVFELOPGASVFVNVTDPSPQVSHGTGFTSFG 257


RESULT 6
A25451
tumor necrosis factor alpha precursor - rabbit
N;Alternate names: cachectin; TNF alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A25454; A25451; JS0727

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R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayaashi, H.
DNA 5, 149-156, 1986
A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabbit
A;Reference number: A25454; MUID:86219711; PMID:3519137
A;Accession: A25454
A;Molecule type: mRNA
A;Residues: 1-234 <ITO>
A;Cross-references: UNIPROT:P04924; GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1986
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A;Reference number: A25451; MUID:86219712; PMID:3519138
A;Accession: A25451
A;Molecule type: DNA
A;Residues: 1-234 <IT2>
A;Note: this sequence differs from that shown in having a Gln inserted between residues 6
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF- α
A;Reference number: JH0309; MUID:91065534; PMID:2249779
A;Accession: JS0727
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62, 'Q', 63-234 <SHA>
A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
C;Genetics:
A;Introns: 62/3; 80/1; 96/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; mem
F;1-81/Domain: propeptide #status predicted <PRO>
F;82-234/Product: tumor necrosis factor #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;147-178/Disulfide bonds: #status predicted

Query Match 9.5%; Score 141; DB 1; Length 234;
Best Local Similarity 22.4%; Pred. No. 0.00017;
Matches 62; Conservative 41; Mismatches 98; Indels 76; Gaps 13;

QY 8 GGPSLGGTCLVLIIFTVLLQSLCVAITYVYFTNELKQMCKYKSGIACFLKEDDSYWD 67
||| : : : : : || || | | | | | | | | | | | | | | | | | | | |
Db 22 GGPGSKRCCLSLFSLL---VAGATTLF-----CLL--HFRVIGP 58
||| : : : : : || || | | | | | | | | | | | | | | | | | | | |
QY 68 NDEESMNSPCWQVKQLRQLVRKMI-LRTSEETISTVQEKQONISPLVRERGPQVAHI 126
: ||| : : : : : ||| : : : : : || | | | | | | | | | | | | | | | |
Db 59 QEEESPNN-----LHLVNPVQMVTLRSRALSD-----KPL-----AHV 94
||| : : : : : || || | | | | | | | | | | | | | | | | | | | |
QY 127 TGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKGFYIYS 186
| : | | | | | | | | | | | | | : : : : : ||| | | | | | | | | | |
Db 95 VA-----NPQVEGQL-----QWLSQRANALLANGMKLTDNLVVPADGLYIYS 138
| : | | | | | | | | | | | | | : : : : : ||| | | | | | | | | | |
QY 187 QTYFRFOEEIKENTKNDKQMVQYIYKY-TSPDPILLMKARNSCWSKDAEYG-----LY 240
| | | : : : : : ||| : : : : : || : : : : : | | | | | | | | | | | |
Db 139 QVLFSGQ-----GCRSYVLLTHTVSRFAVSYPNVKNLLSAIKSPCHRETPEAEPMWYE 193
||| : : : : : || : : : : : || : : : : : | | | | | | | | | | | |
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-PFG 276
||| : : : : : || : : : : : || : : : : : | | | | | | | | | | | |
Db 194 PIYLGGVFQLEKGRDLSTEVNQPEYLDLAESGQVIFG 230
||| : : : : : || : : : : : || : : : : : | | | | | | | | | | | |

RESULT 7
S21738
CD40 ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S21738
R;Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B.N.
; Cosman, D.; Spriggs, M.K.
Nature 357, 80-82, 1992
A;Title: Molecular and biological characterization of a murine ligand for CD40.
A;Reference number: S21738; MUID:92244364; PMID:1374165
A;Accession: S21738
A;Molecule type: mRNA

A;Residues: 1-260 <ARM>	
A;Cross-references: UNIPROT:P27548; EMBL:X65453; NID:g50351; PIDN:CAA46448.1; PID:g50352	
C;Keywords: glycoprotein; transmembrane protein	
F;23-46/Domain: transmembrane #status predicted <TMM>	
F;47-260/Domain: extracellular #status predicted <EXT>	
F;239/Binding site: carbohydrate (Asn) (covalent) #status predicted	
Query Match 9.5%; Score 141; DB 2; Length 260;	
Best Local Similarity 23.5%; Pred. No. 0.0002;	
Matches 59; Conservative 50; Mismatches 104; Indels 38; Gaps 11;	
Qy	17 VLIVIFTVLL--QSLCAVTVYVYFTNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMN 74
Db	23 IFMYLLTVFLITQMIGSVLFAVYLHRRLDKVEEVNLHEDFVFIKKLKRC--NKGEGSL 79
Qy	75 S--PCWQVKQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPQVAAHITGTRGR 132
Db	80 SLLNCEMRQFEDLVKIDITLNK-----EKKENSFEMQRGDEDPQIAAHV----- 125
Qy	133 SNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL-HLRNG-ELVIHEKGFYIYYSQTYF 190
Db	126 ---VSEANSNAASVL-----QW-AKGYTYTMKSNLVMLENGKQLTVKREGLYYVYTVQTF 176
Qy	191 RFQEETIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLYSIQGGIFEL 250
Db	177 CSNRE----PSSQRPFIVGLWLKPSIGSERILLKAANTHSSQLCEQ--QSVHLGGVFEL 230
Qy	251 KENDRIPVSVT 261
Db	231 QAGASVFVNVT 241
RESULT 8	
S17289	
tumor necrosis factor beta precursor - pig	
C;Species: Sus scrofa domestica (domestic pig)	
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004	
C;Accession: S17289	
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.	
Gene 102, 171-178, 1991	
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal	
A;Reference number: S17289; MUID:91340150; PMID:1874444	
A;Accession: S17289	
A;Molecule type: DNA	
A;Residues: 1-204 <KH>	
A;Cross-references: UNIPROT:P26445; EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133	
C;Genetics:	
A;Introns: 32/3; 68/1	
C;Superfamily: tumor necrosis factor	
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage	
F;1-33/Domain: signal sequence #status predicted <SIG>	
F;34-204/Product: tumor necrosis factor beta #status predicted <MAT>	
Query Match 9.1%; Score 134.5; DB 1; Length 204;	
Best Local Similarity 24.7%; Pred. No. 0.00051;	
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;	
Qy	101 STVQEKQONISPLVRERGPQVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS 153
Db	42 SAAQPAHQH-PPKHLARGTLKPAAHLVGDPTDPSLRWRANT-----DRAFLR---- 88
Qy	154 WESSRSGHSFLSNLHLRNGELVTHEKGFYIYYSQTYFRFQEEIKENTKNDKQMVQYIYKY 213
Db	89 -----HGFL----LSNNSLLVPTSGLYFVYSQVVFSGCGFPKATPTPLYLAHEVQLF 137
Qy	214 TS-YDPDILLMKSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEA 272
Db	138 SSQYPHVPPLLSAQKSVCPGQGPW-VRSVYQGAVFLLTQGDQLSTHTDGTPHLLSPSS 196
Qy	273 SFFGAF 278
Db	197 VFFGAF 202

RESULT 9	
S12606	
tumor necrosis factor alpha precursor - pig	
C;Species: Sus scrofa domestica (domestic pig)	
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004	
C;Accession: S12606; S17290; S18965; I46659	
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.	
Nucleic Acids Res. 18, 5564, 1990	
A;Title: Gene sequence of porcine tumor necrosis factor alpha.	
A;Reference number: S12606; MUID:91016861; PMID:2216741	
A;Accession: S12606	
A;Molecule type: DNA	
A;Residues: 1-232 <DRE>	
A;Cross-references: UNIPROT:P23563; EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136	
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.	
Gene 102, 171-178, 1991	
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative analy	
A;Reference number: S17289; MUID:91340150; PMID:1874444	
A;Accession: S17290	
A;Molecule type: DNA	
A;Residues: 1-232 <KH>	
A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134	
A;Note: the authors translated the codon GAG for residue 202 as Gly	
R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.	
submitted to the EMBL Data Library, January 1991	
A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis fac	
A;Reference number: S18965	
A;Accession: S18965	
A;Molecule type: mRNA	
A;Residues: 1-232 <CHO>	
A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138	
R;Pauli, U.; Beutler, B.; Peterhans, E.	
Gene 81, 185-191, 1989	
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction	
A;Reference number: I46659; MUID:90034181; PMID:2478420	
A;Accession: I46659	
A;Status: preliminary; translated from GB/EMBL/DBBJ	
A;Molecule type: mRNA	
A;Residues: 44-232 <PAU>	
A;Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695	
C;Genetics:	
A;Introns: 62/3; 78/1; 93/1	
C;Superfamily: tumor necrosis factor	
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myrie	
F;1-77/Domain: propeptide #status predicted <PRO>	
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>	
F;19,20/Binding site: myristate (Iys) (covalent) #status predicted	
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted	
F;144-176/Disulfide bonds: #status predicted	
Query Match 9.0%; Score 133; DB 1; Length 232;	
Best Local Similarity 21.3%; Pred. No. 0.00082;	
Matches 61; Conservative 40; Mismatches 100; Indels 86; Gaps 11;	
Qy	2 AMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVTVYVYFTNELKQMDKYSKSGIACFLKED 61
Db	16 ALAKKAGGPQGSRRCLCLSLFSFLL---VAGATTLF-----CLLHFE 54
Qy	62 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPQR 121
Db	55 --VIGPQKEEFPAGPL-----SINPLAQ----- 75
Qy	122 VAAHITGRGRSNTLSSPNS---KNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHE 178
Db	76 -----GLRSSQTS DKPVAHVAVNVKAEGQL--QWQSGYANALLANGVKLKNQLVVP 127
Qy	179 KGFYIYSQTYFRFQEEIKEN---TKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSK-- 233
Db	128 DGLYLIYSQVLFRRGGCPSTNVFLTHTISRIA-----VSYQTKVNLLSAIKSPCQRETP 181
Qy	234 ---DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276

Db 182 EGAEAKPWEPIYLGGVFQLEKODRLSABINLPDYLDFAESGQVYFG 228

RESULT 10

S22052

tumor necrosis factor alpha precursor - baboon

C;Species: Papio sp. (baboon)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S22052

R;Sanjanwala, M.; Edwards, A.

submitted to the EMBL Data Library, September 1991

A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A;Reference number: S22052

A;Accession: S22052

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-233 <SAN>

A;Cross-references: UNIPROT:P33620; EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160

C;Genetics:

A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 8.9%; Score 131.5; DB 1; Length 233;

Best Local Similarity 19.2%; Pred. No. 0.0011;

Matches 55; Conservative 49; Mismatches 98; Indels 85; Gaps 10;

Qy 2 AMMEVQGPSLGGTQCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKED 61

Db 16 ALPKKTGGQSRRCFLSLFSLLVAGATTLFCLLHFGVIGPQREFPK----- 65

Qy 62 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNISPLVRERGPQR 121

Db 66 ---DP----SLISPLAQA-----VRSSRTPS-----DK 87

Qy 122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 181

Db 88 PVAHVVA-----NPQAEQGL--QWLNRANALLANGVELRDNLQVVPSEGL 131

Qy 182 YYYISQTYFRFQEEIKENTKNDKQMVQYIYKYT-----SYDPILLMKSAARNSCWSK-- 233

Db 132 YLIYSQVLEFKGQ-----GCPSTHVLLTHTISRIVASYQTKVNLLSAIKSPCQRETP 182

Qy 234 ---DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276

Db 183 EGAEAKPWEPIYLGGVFQLEKGDRLSABINLPDYLDFAESGQVYFG 229

RESULT 11

JQ1344

tumor necrosis factor alpha precursor - horse

N;Alternate names: cachectin; TNF alpha

C;Species: Equus caballus (domestic horse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JQ1344

R;Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f

A;Reference number: JQ1344; MUID:92084125; PMID:1748301

A;Accession: JQ1344

A;Molecule type: DNA

A;Residues: 1-234 <SUX>

A;Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245

C;Comment: This protein is an important proximal mediator of endotoxemia.

C;Genetics:

A;Gene: TNF-alpha

A;Introns: 62/3; 79/1; 95/1

C;Superfamily: tumor necrosis factor

C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb

F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;146-178/Disulfide bonds: #status predicted

Query Match 8.9%; Score 131; DB 1; Length 234;

Best Local Similarity 20.8%; Pred. No. 0.0012;

Matches 60; Conservative 40; Mismatches 89; Indels 100; Gaps 13;

Qy 8 GGPSLGGTQCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFL-----K 59

Db 22 GGPGSRRCLCLSLFSLL----VAGATTLF-----CLLHFGVIGPQR 60

Qy 60 EDDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNISPLVRERGP 119

Db 61 EEQL---PNAFQSIN-PLAQT-----LRSSRTPS----- 86

Qy 120 ORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHK 179

Db 87 DKPVAHVVA-----NPQAEQGL--QWLSGRANALLANGVKLTDNLQVPLD 130

Qy 180 GFYYISQTYFRFQEEIKENTKNDKQMVQYIYKYT-----SYDPILLMKSAARNSCWSK 233

Db 131 GLYLIYSQVLEFKGQ-----GCPSTHVLLTHTISRIVASYPSKVNLLSAIKSPCHTE 181

Qy 234 DAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276

Db 182 SPEQAEAKPWEPIYLGGVFQLEKGDLSAEINQPNYLDFAESGQVYFG 230

RESULT 12

S24642

tumor necrosis factor alpha precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: I46047; S24642

R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tun

A;Reference number: I46046; MUID:94083525; PMID:8260599

A;Accession: I46047

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-233 <CL2>

A;Cross-references: UNIPROT:Q06599; EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C;Genetics:

A;Gene: TNFA

A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 8.8%; Score 130.5; DB 1; Length 233;

Best Local Similarity 20.3%; Pred. No. 0.0013;

Matches 59; Conservative 43; Mismatches 95; Indels 93; Gaps 13;

Qy 3 MMEVQGPSLGGTQCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFL---- 58

Db 17 LSEKAGGPGQSRSCCLSLFSLL----VAGATTLF-----CLLHFGV 55

Qy 59 ---KEDDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNISPLVR 115

Db 56 IGPQREESPGP---SINSPLVQT-----LRSSSQASS----- 85

Qy 116 ERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 175

Db 86 ----NKPVAHVVA-----DINSPGQLR-----WWDSYANALMANGVKLEDNLV 125

Qy 176 IHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK--YTSYDPDILLMKSAARNSC--- 230

Db 126 VPADGLYLIYSQVLEFRGQ-----GCPSTPLFLTHTISRIVASYQTKVNLLSAIKSPCHRE 180

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 06:07:44 ; Search time 176 Seconds
(without alignments)
817.581 Million cell updates/sec

Title: US-10-662-431-2
Perfect score: 1478
Sequence: 1 MAMMEVQGPGSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1478	100.0	281	1	TN10_HUMAN	P50591 homo sapien
2	963	65.2	287	2	Q8K3G0	Q8k3g0 rattus norv
3	930	62.9	291	1	TN10_MOUSE	P50592 mus musculus
4	809.5	54.8	304	2	Q7T1F2	Q7t1f2 gallus gall
5	577.5	39.1	299	2	Q6DHG9	Q6dHg9 brachydanio
6	334.5	22.6	317	2	Q7ZYX9	Q7zyx9 brachydanio
7	307.5	20.8	287	2	Q90WT9	Q90wt9 gallus gall
8	305.5	20.7	214	2	Q9DDZ5	Q9ddz5 brachydanio
9	291	19.7	63	2	Q6JSD9	Q6jsd9 homo sapien
10	267.5	18.1	318	1	TN11_RAT	Q9ese2 r tumor nec
11	258.5	17.5	316	1	TN11_MOUSE	O35235 m tumor nec
12	251.5	17.0	317	1	TN11_HUMAN	O14788 h tumor nec
13	189.5	12.8	279	1	TNF6_MOUSE	P41047 mus musculus
14	187	12.7	280	1	TNF6_CERTO	Q9bdn1 cercocebus
15	186	12.6	281	1	TNF6_HUMAN	P48023 homo sapien
16	185	12.5	280	1	TNF6_MACPA	P63308 macaca fasc
17	185	12.5	280	1	TNF6_MACMU	P63307 macaca mula
18	185	12.5	280	1	TNF6_MACNE	P63306 macaca neme
19	184.5	12.5	279	2	Q7TMV9	Q7tmv9 mus musculus
20	184	12.4	272	1	TNF5_CHICK	Q9i8d8 gallus gall
21	182	12.3	282	1	TNF6_PIG	Q9bea8 sus scrofa
22	180	12.2	252	2	Q8K3Y8	Q8k3y8 mus musculus
23	178.5	12.1	280	2	Q861W5	Q861w5 felis silve
24	177.5	12.0	278	1	TNF6_RAT	P36940 rattus norv
25	175.5	11.9	169	2	Q9WV90	Q9wv90 marmota mon
26	175	11.8	252	2	Q80YZ0	Q80yz0 mus musculus
27	173	11.7	252	2	Q8K3Y7	Q8k3y7 rattus norv
28	166	11.2	251	2	Q8NFE9	Q8nfe9 homo sapien
29	164	11.1	261	1	TNF5_BOVIN	P51749 bos taurus
30	163.5	11.1	131	2	Q6J3Q6	Q6j3q6 canis famil
31	160	10.8	174	1	TN15_HUMAN	O95150 homo sapien

RESULT 1
TN10_HUMAN
ID TN10_HUMAN STANDARD; PRT; 281 AA.
AC P50591;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
GN Name=TNFSF10; Synonyms=APO2L, TRAIL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF family
RT that induces apoptosis.";
RL Immunity 3:673-682(1995).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96278649; PubMed=8663110; DOI=10.1074/jbc.271.22.12687;
RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
RA Ashkenazi A.;
RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
RT necrosis factor cytokine family.";
RL J. Biol. Chem. 271:12687-12690(1996).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

043557 homo sapien
Q8mj19 macaca mula
Q7t2q3 cyprinus ca
Q9gyh9 mus musculus
Q9bdn3 callithrix
Q9bdm3 actus trivi
Q97605 felis silve
Q6u817 lateolabrax
P63305 cercocebus
P63304 macaca mula
Q97626 canis famil
P29965 homo sapien
O70332 mesocricetu
Q95mq5 sus scrofa

32 159.5 10.8 240 1 TN14_HUMAN
33 157 10.6 154 2 Q8MJ19
34 153.5 10.4 227 2 Q7T2Q3
35 152.5 10.3 239 1 TN14_MOUSE
36 152 10.3 261 1 TNF5_CALJA
37 150.5 10.2 261 1 TNF5_AOTFR
38 149.5 10.1 260 1 TNF5_FELCA
39 149 10.1 241 2 Q6U817
40 148 10.0 261 1 TNF5_CERTO
41 148 10.0 261 1 TNF5_MACMU
42 147.5 10.0 260 1 TNF5_CANFA
43 147.5 10.0 261 1 TNF5_HUMAN
44 144.5 9.8 216 2 O70332
45 143 9.7 261 1 TNF5_PIG

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[4]

RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.

RX MEDLINE=20017054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80207-5;

RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,

RA Kelley R.F., Ashkenazi A., de Vos A.M.;

RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a

RL complex with death receptor 5.";

RL Mol. Cell 4:563-571(1999).

[5]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.

RX PubMed=10542098; DOI=10.1038/14935;

RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,

RA Jones E.Y., Screaton G.R.;

RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring

RT specificity in apoptotic initiation.";

RL Nat. Struct. Biol. 6:1048-1053(1999).

[6]

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.

RX MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;

RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,

RA Sung Y.C., Oh B.-H.;

RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with

RT selective antitumor activity.";

RL Immunity 11:253-261(1999).

CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,

CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and

CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity

CC may be modulated by binding to the decoy receptors

CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot

CC induce apoptosis.

CC -!- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per

CC trimer.

CC -!- SUBUNIT: Homotrimer.

CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung

CC and prostate.

CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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CC or send an email to license@isb-sib.ch).

DR EMBL; U37518; AAC50332.1; -.

DR EMBL; U57059; AAB01233.1; -.

DR EMBL; BC032722; AAH32722.1; -.

DR PDB; 1D0G; X-ray; A/B/D=114-281.

DR PDB; 1D2Q; X-ray; A=114-281.

DR PDB; 1D4V; X-ray; B=119-281.

DR PDB; 1DG6; X-ray; A=91-281.

DR PDB; 1DU3; X-ray; D/E/F/J/K/L=114-281.

DR Genew; HGNC:11925; TNFRSF10.

DR H-InvDB; HIX0003863; -.

DR MIM; 603598; -.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0005625; C:soluble fraction; TAS.

DR GO; GO:0005102; F:receptor binding; TAS.

DR GO; GO:0007267; P:cell-cell signaling; TAS.

DR GO; GO:0006917; P:induction of apoptosis; TAS.

DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IEP.

DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR006052; TNF_family.

DR InterPro; IPR008983; TNF_like.

DR InterPro; IPR003636; TNF_subf.

DR Pfam; PF00229; TNF; 1.

DR ProDom; PD002012; TNF_subf; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS50049; TNF 2; 1.

KW 3D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor;

KW Transmembrane; Zinc.

FT DOMAIN 1 17 Cytoplasmic (Potential).

FT TRANSMEM 18 38 Signal-anchor for type II membrane

FT protein (Potential).

FT Extracellular (Potential).

FT Zinc.

FT DOMAIN 39 281

FT METAL 230 230

FT STRAND 123 127

FT STRAND 149 150

FT STRAND 163 165

FT STRAND 167 170

FT TURN 171 172

FT STRAND 173 176

FT STRAND 180 193

FT TURN 198 199

FT STRAND 205 213

FT STRAND 220 228

FT TURN 233 234

FT STRAND 237 250

FT TURN 252 253

FT STRAND 255 260

FT HELIX 263 265

FT STRAND 266 267

FT TURN 270 272

FT STRAND 274 279

SQ SEQUENCE 281 AA; 32509 MW; DDAAAF78DAAB2F6D CRC64;

Query Match 100.0%; Score 1478; DB 1; Length 281;

Best Local Similarity 100.0%; Pred. No. 4.4e-113;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120

Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120

Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180

Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180

Qy 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNSCWSKDAEYGLY 240

Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 2

Q8K3G0

ID Q8K3G0 PRELIMINARY; PRT; 287 AA.

AC Q8K3G0;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE TNF-related apoptosis inducing ligand.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DA;

RA Mueller A.M., Giegerich G.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY115578; AAM49797.1; -.

DR HSSP; P50591; 1D2Q.

DR GO; GO:0016020; C:membrane; IEA.

```
DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; UNKNOWN_1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;

Query Match 65.2%; Score 963; DB 2; Length 287;
Best Local Similarity 67.7%; Pred. No. 8.5e-71;
Matches 189; Conservative 29; Mismatches 51; Indels 10; Gaps 3;

QY 9 GPSLQG----TCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGIACFLKEDDSY 64
Db 9 GPSFSQHFTMTVICIVLLQVLLQALTVAVTMYFENNEVKQLQDNYSKIGLACFSKEDGDF 68

QY 65 WDPNDEESMNSPCWQVKQLRQVRKMLRTSEETISTVQEQQNISPLVRERGQPVAA 124
Db 69 WDSDEGILNRPCLQVKRQLYQLIEEVLRTFEKTIISTVPEKQLSTPPLPRGRRPQVAA 128

QY 125 HITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYI 184
Db 129 HITGITRRSNLALIPISKDGLTQKIETWESSRRGHSLNHLRNGELVIQEEGLYI 188

QY 185 YSQTYFRFQE--EIKENTKND----KQMVQYIYKYTSYDPDILLMKARNCSWKSDAEYG 238
Db 189 YSQTYRFEKAEBASKTVSKOGGRKQMVQYIYKYTSYDPDILLMKARNCSWREAEYG 248

QY 239 LYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGA 277
Db 249 LYSIQGGIFELKENDRIFVSVTNEHLMDLDHEASFFGA 287

RESULT 3
TN10 MOUSE
ID TN10 MOUSE STANDARD; PRT; 291 AA.
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein).
GN Name=Tnfsf10; Synonyms=Trail;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF family
RT that induces apoptosis.";
RL Immunity 3:673-682(1995).
CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC may be modulated by binding to the decoy receptors
CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC induce apoptosis.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Widespread.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
DR EMBL; U37522; AAC52345.1; -.
DR HSSP; P50591; 1D2Q.
DR MGD; MGI:107414; Tnfsf10.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Apoptosis; Cytokine; Signal-anchor; Transmembrane.
FT DOMAIN 1 17 Cytoplasmic (Potential).
FT TRANSMEM 18 38 Signal-anchor for type II membrane
FT 39 291 protein (Potential).
FT DOMAIN 39 291 Extracellular (Potential).
FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 62.9%; Score 930; DB 1; Length 291;
Best Local Similarity 65.6%; Pred. No. 4.4e-68;
Matches 177; Conservative 37; Mismatches 50; Indels 6; Gaps 1;

QY 17 VLIVIFTVLLQSLCVAVTVYFTNELKQMDKYSGIACFLKEDDSYWDPNDEESMNSP 76
Db 21 ICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSKTDDEFDWSTDGEILNRP 80

QY 77 CWQVKWQLRQLVRKMLRTSEETISTVQEQQNISPLVRERGQPVAAHITGTRGRSNTL 136
Db 81 CLQVKRQLYQLIEEVLRTFDQTIISTVPEKQLSTPPLPRGGRPQKVAHITGITRRNSA 140

QY 137 SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYIYYSQTYFRFQEE- 195
Db 141 LIPISKDGLTQKIESWESSRSGHSFLNHLRNGELVIEQEGLYIYYSQTYFRFQEA 200

QY 196 ----IKENTKNDKQMVQYIYKYTSYDPDILLMKARNCSWKSDAEYGLYSIQGGIFEL 250
Db 201 DASKMVSCKDKVRTKQLVQYIYKYTSYDPDIPVLMKARNCSWRSRDAEYGLYSIQGGIFEL 260

QY 251 KENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
Db 261 KGNDRIFVSVTNEHLMDLDQEAFFGAFLI 290

RESULT 4
Q7T1F2
ID Q7T1F2 PRELIMINARY; PRT; 304 AA.
AC Q7T1F2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor necrosis factor related apoptosis inducing ligand.
GN Name=TRAIL;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Sayed A.A., Horiuchi H., Furusawa S., Matsuda H.;
RT "Molecular Cloning and Characterization of Chicken Tumor Necrosis
RT Factor (TNF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis
RT Inducing Ligand (TRAIL).";
RL J. Vet. Med. Sci. 66:643-650(2004).
DR EMBL; AB114678; BAC79267.1; --
```

DR HSSP; P50591; 1D2Q.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 54.8%; Score 809.5; DB 2; Length 304;
Best Local Similarity 55.4%; Pred.No. 3.6e-58;
Matches 160; Conservative 45; Mismatches 65; Indels 19; Gaps 6;

Qy 8 GGPSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKEDDSYWD 67
Db 5 GGPSPAHTCGAVLVAALLQSVCAVTVYFTNELKQLWDYTSRSGTACLTGEELGDLIQ 64

Qy 68 N-----DEESMNSPCWQKWQLRQLVRKMILRTSEETISTVQ-EKQONISPLVRERGPO- 120
Db 65 NLDVVBESKDRVADPCWQVKHLGKLTKQWMSRILQENMSAINGDRTQALS--RDEPPQG 122

Qy 121 ---RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH 177
Db 123 PTLRIAHLTGSSKRSSA-SPHNVLSYRGIGHKIHSWESSRRGHSLYNVELWNGELVVP 181

Qy 178 EKGFFYYISQTYFRFQEE-----IKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCW 231
Db 182 QTGFYYIISQTYFRFRENEDSDGLLERIKNPKQLVQYIYKLTNYDPDPILLMKSARTSCW 241

Qy 232 SKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
Db 242 SKKAEYGLYSVYQGGVFLKREDRIFVSVNSDSIDVMDKEASFFGAFMI 290

RESULT 5
Q6DHG9 PRELIMINARY; PRT; 299 AA.
AC Q6DHG9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Zgc:92320.
GN Name=zgc:92320;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076005; AAH76005.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 299 AA; 33526 MW; BA776793D2F11ED5 CRC64;

Query Match 39.1%; Score 577.5; DB 2; Length 299;
Best Local Similarity 42.2%; Pred.No. 3.9e-39;
Matches 121; Conservative 57; Mismatches 82; Indels 27; Gaps 8;

Qy 18 LIVIFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKED---DSYWDPNDEESMN 74
Db 15 LLLAAAILQTIAVAVTFIYFSNVLSMTKETFSKSSVCLMRANLRTIKQELNGAEGKD 74

Qy 75 SPQWQVKQLRQLVRK-MILRTSEETISTVQEKQONISPLV-----RERGQRVAAHITG 128
Db 75 DPCWQVQQLHFLIEKSMSSRYQKEITSAVKDEVSRVLPISLVIQDQEDSSRPKIAAHVTG 134

Qy 129 TRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQT 188
Db 135 SYTPESEKDGAGLPNRKVYQGIQSWSEK-GLAFLQNVELSDGELVVPQAGLYIYSQT 193

Qy 189 YFR---FQEEIKENTKND-----KQMVQYIY-KYTSYDPDPILLMKSARNSCWSK 233
Db 194 YFRHTLIEED--ESAREDEYCSMGESVRGKPMQLQYVYKKVSSYQVPILLMKNARTTCWSR 251

Qy 234 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
Db 252 DSEYGLYSIYQAGLFQLGSGDRVFTVSVNSVTIDMDEKSFFGAFLV 298

RESULT 6
Q7ZYX9 PRELIMINARY; PRT; 317 AA.
AC Q7ZYX9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tnfsf101 protein.
GN Name=tnfsf101;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,


```
RESULT 14
TNF6_CERTO          STANDARD;          PRT;    280 AA.
AC Q9BDN1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN Name=TNFSF6; Synonyms=CD95L, FASL;
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC modulates its effects (By similarity).
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF344847; AAK37606.1; -.
DR HSSP; P50591; 1D2Q.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
FT CHAIN          1      280      Tumor necrosis factor ligand superfamily
FT                  member 6, membrane form.
FT CHAIN          129    280      Tumor necrosis factor ligand superfamily
FT                  member 6, soluble form (By similarity).
FT DOMAIN          1      80      Cytoplasmic (Potential).
FT TRANSMEM       81    101      Signal-anchor for type II membrane
FT                  protein (Potential).
FT DOMAIN          102    280      Extracellular (Potential).
FT DOMAIN          4      69      Pro-rich.
FT DOMAIN          45    64      Poly-Pro.
FT SITE           128    129      Cleavage (By similarity).
FT DISULFID       201    232      Potential.
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FT CARBOHYD      183      N-linked (GlcNAc. .) (Potential).
FT CARBOHYD      249      N-linked (GlcNAc. .) (Potential).
FT CARBOHYD      259      N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE      280 AA; 31407 MW; 729EA60067B7D398 CRC64;

Query Match          12.7%; Score 187; DB 1; Length 280;
Best Local Similarity 22.1%; Pred. No. 4e-07;
Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;

QY 4 MEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKEDDS 63
   :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 70 LKKGHNHSTG-LCLLVMFVVALVGLGLGMFQLFHLQKELAE-----LRESTS 118
   :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 64 YWDPNDEESMNSPCWQVKWQLRQLVRKMLTSEETISTVQEKQQNISPLVRERGQ RVA 123
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 119 -----QKHTASSLEKQIGHPSPPPEKKEQRKV 145

QY 124 AHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFY 183
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 146 AHLTG-----KPNRSRSMPL-----EWEDT-YGIVLLSGVKYKGGGLVINETGLYF 189
   :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 184 IYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYDPDILLMKSAARNSCWSKDAEYGLYSI 242
   :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 190 VYSKVYFRGQ-----SCTNLPLSHKVMYMRNSKYPQDLVMMEGKMMS-YCTTGQMWAHSS 242

QY 243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFFGAF 278
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 243 YLGAVFNLTSTDHLYVNVSELSLVNPFESQTFFGLY 278

RESULT 15
TNF6_HUMAN          STANDARD;          PRT;    281 AA.
AC P48023; Q9BZP9;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (Apoptosis antigen ligand) (APTL) (CD178 antigen).
GN Name=TNFSF6; Synonyms=APTLGL1, FASL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
RT lymphocytes.";
RL J. Exp. Med. 181:71-77(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: gene structure, chromosomal location and species
RT specificity.";
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Schaeetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,
RA Fusamoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT infection.";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
```

RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT "Isolation and characterization of a new naturally occurring variant of
RT human Fas ligand that is expressed only in membrane bound form.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshilyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
RX MEDLINE=97373583; PubMed=9228058; DOI=10.1074/jbc.272.30.18827;
RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
RA Tersikh A., Peitsch M.C., Tschoopp J.;
RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
RL J. Biol. Chem. 272:18827-18833(1997).
RN [10]
RP PROCESSING.
RX MEDLINE=98087475; PubMed=9427603;
RA Tanaka M., Itai T., Adachi M., Nagata S.;
RT "Downregulation of Fas ligand by shedding.";
RL Nat. Med. 4:31-36(1998).
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/Dcr3
CC modulates its effects.
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released
CC into the extracellular fluid, probably by cleavage form the cell
CC surface.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P48023-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P48023-2; Sequence=VSP_006443, VSP_006444;
CC -!- PTM: N-glycosylated.
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing.
CC -!- DISEASE: Defects in TNFSF6 are a cause of autoimmune
CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome

CC involving hemolytic anemia and thrombocytopenia with massive
CC lymphadenopathy and splenomegaly.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X89102; CAA61474.1; -;
DR EMBL; U08137; AAC50071.1; -;
DR EMBL; U11821; AAC50124.1; -;
DR EMBL; D38122; BAA07320.1; -;
DR EMBL; AF288573; AAG60017.1; -;
DR EMBL; Z96050; CAB09424.1; -;
DR EMBL; BC017502; AAH17502.1; -;
DR EMBL; AB013303; BAA32542.1; -;
DR PIR; I38707; I38707.
DR HSSP; P50591; 1D2Q.
DR Genew; HGNC:11936; TNFSF6.
DR H-InvDB; HIX0001337; -;
DR MIM; 134638; -;
DR MIM; 601859; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005102; P:receptor binding; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB kinase; IEP.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008064; Fas_ligand.
DR InterPro; IPR006053; TNF_abs.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Alternative splicing; Antigen; Apoptosis; Cytokine; Glycoprotein;
KW Signal-anchor; Transmembrane.
FT CHAIN 1 281 Tumor necrosis factor ligand superfamily
FT member 6, membrane form.
FT CHAIN 130 281 Tumor necrosis factor ligand superfamily
FT member 6, soluble form.
FT DOMAIN 1 80 Cytoplasmic (Potential).
FT TRANSMEM 81 102 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 103 281 Extracellular (Potential).
FT DOMAIN 4 70 Pro-rich.
FT DOMAIN 45 65 Poly-Pro.
FT SITE 129 130 Cleavage.
FT DISULFID 202 233 Potential.
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 250 250 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 260 260 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 117 127 STSQMHTASSL -> ATPVHPLKKRS (in isoform
FT 2).
FT /FTId=VSP_006443.
FT Missing (in isoform 2).
FT /FTId=VSP_006444.
FT P->D,F,R: Lowers binding to TNFRSF6 and
FT reduces cytotoxicity more than 100-fold.
FT Y->F,R: Lowers binding to TNFRSF6 and
FT abolishes cytotoxicity.
FT F->L: Abolishes binding to TNFRSF6 and
FT cytotoxicity.
FT

```
SQ SEQUENCE 281 AA; 31485 MW; A8A6EB358246E9BB CRC64;
Query Match 12.6%; Score 186; DB 1; Length 281;
Best Local Similarity 22.1%; Pred. No. 4.9e-07;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

QY 4 MEVQGGPSLQGTCLIVIFTVLLQSLCVAV---TYVYFTNELKQMDKYKSGIACFLKE 60
   : : | | | | : : | | : : | | : : | | : : | | : : | | : :
Db 71 LKGRGNHSTG-LCLLVMFMMVLVALVGLGMFQLFHLQELAEIARESTSQMHTASSLEK 129
   : : | | | | : : | | : : | | : : | | : : | | : : | | : :

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQQNISPLVRERGPO 120
   : : | | | | : : | | : : | | : : | | : : | | : : | | : :
Db 130 QIGHPSPPPE-----KKELRKV----- 146

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
   | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 147 ---AHLT---GKSNRSRMP-----LEWEDT-YGIVLLSGVKYKKGGLVINETG 187

QY 181 FYIYISQYFRFPQEEIKENTKNDKQMVQYIY-KYTSYDPDPIILLMKSARNS-----CWSK 233
   | : | | : | | | : | | : | | : | | : | | : | | : | | : |
Db 188 LYFVYSKVYFRGQ-----SCNNPLPSHKVYMRNSKYPQDLVMEGKMMSYCTTGQMMWAR 241

QY 234 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
   | | | | : | | : | | : | | : | | : | | : | | : | | : |
Db 242 -----SSYLGAVFNLTSADHLYVNVVSELSLVNFEEESQTFFFGLY 279
```

Search completed: June 3, 2005, 06:24:55
Job time : 178 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 11:54:33 ; Search time 162 Seconds
(without alignments)
670.862 Million cell updates/sec

Title: US-10-662-431-2
Perfect score: 1478
Sequence: 1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAPLVG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 55

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	2	AAW19777 Novel cyt
2	1478	100.0	281	2	AAW27134 Human Apo
3	1478	100.0	281	2	AAW19787 Human apo
4	1478	100.0	281	2	AAW76829 Human TL2
5	1478	100.0	281	2	AAW56760 Human TRA
6	1478	100.0	281	2	AAW44354 Human AGP
7	1478	100.0	281	2	AAY01517 Protein a
8	1478	100.0	281	2	AAY27012 Human Apo
9	1478	100.0	281	3	AAY81956 Human Apo
10	1478	100.0	281	3	AAB24038 Human PRO
11	1478	100.0	281	3	AAB08545 Amino aci
12	1478	100.0	281	3	AAB28691 Human AGP
13	1478	100.0	281	4	AAB50977 Human PRO
14	1478	100.0	281	4	AAB67243 Human Apo
15	1478	100.0	281	4	AAE11031 Human TNF
16	1478	100.0	281	4	AAB48350 Human TL2
17	1478	100.0	281	5	ABB08133 Human TRA
18	1478	100.0	281	5	ABG31630 Human TRA
19	1478	100.0	281	5	AAU75062 Human TNF
20	1478	100.0	281	5	AAM51077 Human Apo
21	1478	100.0	281	5	ABP51954 Human Apo
22	1478	100.0	281	5	AAO19095 C neoform
23	1478	100.0	281	5	AAU79593 Human TNF
24	1478	100.0	281	6	ABG73861 Human Apo
25	1478	100.0	281	6	ABU10205 Human Apo

26	1478	100.0	281	6	ABU71443 Human neo
27	1478	100.0	281	6	ABG72738 Human TNF
28	1478	100.0	281	6	AAO29543 Human TRA
29	1478	100.0	281	6	ABU08558 Human TNF
30	1478	100.0	281	6	ABR42313 Human TRA
31	1478	100.0	281	6	ABG71905 Human TRA
32	1478	100.0	281	6	ABP60546 Human tum
33	1478	100.0	281	6	AAE36258 Human TR4
34	1478	100.0	281	6	AAO31151 Human TNF
35	1478	100.0	281	6	ABO25125 Human TNF
36	1478	100.0	281	7	ADB61471 Native hu
37	1478	100.0	281	7	ADC35202 Human TNF
38	1478	100.0	281	7	ADD14080 Human src
39	1478	100.0	281	7	ADD19010 Human dis
40	1478	100.0	281	7	ABW02276 Human TRA
41	1478	100.0	281	8	ADE76953 Human pro
42	1478	100.0	281	8	ADK72311 Human Apo
43	1478	100.0	281	8	ADK72303 Human Apo
44	1478	100.0	281	8	ADK72304 Human Apo
45	1478	100.0	281	8	ADK72296 Human wil
46	1478	100.0	281	8	ADK72310 Human Apo
47	1478	100.0	281	8	ADJ63976 Human apo
48	1478	100.0	281	8	ADL71816 Human apo
49	1478	100.0	281	8	ADK15498 Human TRA
50	1478	100.0	281	8	ADN07587 Human apo
51	1478	100.0	281	8	ADR14209 Human NF-
52	1478	100.0	281	8	ADK82215 Human TRA
53	1478	100.0	281	8	ADS88000 Tumour tr
54	1478	100.0	281	8	ABO84415 Human can
55	1478	100.0	281	8	ADP23388 PRO polyp

ALIGNMENTS

RESULT 1	
AAW19777	
ID	AAW19777 standard; protein; 281 AA.
XX	
AC	AAW19777;
XX	
DT	22-SEP-1997 (first entry)
XX	
DE	Novel cytokine Apo-2 ligand.
XX	
KW	Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1. .281
FT	/note= "Claim 4"
FT	Region 1. .14
FT	/label= Cytoplasmic_region
FT	Protein 15. .281
FT	/note= "Claim 3"
FT	Region 15. .40
FT	/label= Transmembrane_region
FT	Protein 41. .281
FT	/note= "Claim 2"
FT	Region 41. .281
FT	/label= Extracellular_region
FT	Modified-site 109
FT	/label= Glycosylation
FT	/note= "putative N-linked glycosylation site"
FT	Protein 114. .281
FT	/note= "Claim 1"
XX	
PN	WO9725428-A1.
XX	
PD	17-JUL-1997.
XX	
PF	08-JAN-1997; 97WO-US000272.

XX 09-JAN-1996; 96US-00584031.
PR (GETH) GENENTECH INC.
XX Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX WPI; 1997-372867/34.
DR N-PSDB; AAT72796.
XX Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
PT apoptosis for the treatment of breast and colon cancer.
XX Claim 4; Fig 1a; 72pp; English.
XX A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian
CC cell apoptosis. It is believed to be a member of the tumour necrosis
CC factor cytokine family. Its amino acid sequence was deduced from a cDNA
CC clone (AAT72796) isolated from a human placental cDNA library. Apo-2
CC ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
CC 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
CC transformed or transfected with a vector contg. Apo-2 ligand nucleic
CC acid. They can be used to induce apoptosis in mammals and to treat
CC pathological conditions such as cancer (esp. breast or colon cancer) or
CC to raise antibodies useful in diagnostic assays
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCWQVKQLRQVRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQVRKMILRTSEETISTVQEKQONISPLVRERGPQ 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180

Qy 181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 2
AAW27134
ID AAW27134 standard; protein; 281 AA.
XX
AC AAW27134;
XX
DT 02-APR-1998 (first entry)
XX
DE Human Apoptosis inducing molecule-I (AIM-I).
XX
KW Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
KW tumour necrosis factor ligand superfamily; AIM-I altered expression;
KW neoplasia inhibition; anti-inflammatory agent.
XX
OS Homo sapiens.
XX
PN WO9733899-A1.
XX
PD 18-SEP-1997.
XX

PF 14-MAR-1996; 96WO-US003773.
XX
PR 14-MAR-1996; 96WO-US003773.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM;
XX
DR WPI; 1997-470807/43.
DR N-PSDB; AAT85210.
XX
PT New isolated apoptosis inducing molecule-I - used to develop products for
PT the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
PT versus host disease or inflammation.
XX
PS Claim 2; Fig 1; 82pp; English.
XX
CC The present sequence represents a human Apoptosis inducing molecule-I
CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand
CC superfamily. The products can be used in the diagnosis and treatment of
CC disorders related to under-expression, over-expression or altered
CC expression of AIM-I. AIM-I or agonists can be used for treating
CC autoimmune disorders including systemic lupus erythematosus,
CC immunoproliferative disease lymphadenopathy (IPL),
CC angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit
CC neoplasia such as tumour cell growth, to treat restenosis, to regulate
CC haematopoiesis in endothelial cell development, to stimulate peripheral
CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or
CC osteoporosis, for preventing graft-host rejection, and as anti-
CC inflammatory agents, for treating endotoxic shock or to prevent
CC activation of HIV
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCWQVKQLRQVRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQVRKMILRTSEETISTVQEKQONISPLVRERGPQ 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180

Qy 181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 3
AAW19787
ID AAW19787 standard; protein; 281 AA.
XX
AC AAW19787;
XX
DT 24-SEP-1997 (first entry)
XX
DE Human apoptosis inducer cytokine TRAIL.
XX
KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;

KW thrombotic microangioplasty; therapy.

XX Homo sapiens.

OS

XX

FH Key Location/Qualifiers

FT Domain 1. .18

FT /label= Cytoplasmic_domain

FT Domain 19. .38

FT /label= Transmembrane_domain

FT Domain 39. .281

FT /label= Extracellular_domain

FT /note= "contains a receptor-binding region"

FT Cleavage-site 89. .90

FT /note= "potential KEX2 protease processing site"

FT Modified-site 109. .111

FT /note= "potential N-glycosylation site"

FT Cleavage-site 149. .150

FT /note= "potential KEX2 protease processing site"

XX

PN WO9701633-A1.

XX

PD 16-JAN-1997.

XX

PF 25-JUN-1996; 96WO-US010895.

XX

PR 29-JUN-1995; 95US-00496632.

PR 01-NOV-1995; 95US-00548368.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Wiley SR, Goodwin RG;

XX

DR WPI; 1997-118715/11.

DR N-PSDB; AAT72847.

XX

PT TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected

PT cells - useful for treating thrombotic microangiopathy, cancer and viral

PT infection and for use in assays.

XX

PS Claim 10; Page 43-44; 62pp; English.

XX

CC Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)

CC (AAW19787) is a novel cytokine that induces apoptosis of certain target

CC cells, including cancer cells and virally infected cells. Its amino acid

CC sequence was deduced from cDNA clone HuA1C (AAT72848), deposited in

CC vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble

CC polypeptides) can be expressed in host cells and used in the treatment of

CC cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or

CC to raise antibodies that may be useful for treating thrombotic

CC microangiopathies

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNCSWSDAEYGLY 240

DB 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNCSWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 4

AAW76829

ID AAW76829 standard; protein; 281 AA.

XX

AC AAW76829;

XX

DT 25-JAN-1999 (first entry)

XX

DE Human TL2 protein.

XX

KW TR6; tumour necrosis factor related receptor; human; treatment; stroke;

KW inflammation; arthritis; septicaemia; autoimmune disease; restenosis;

KW transplant rejection; infection; ischaemia; brain injury; bone disease;

KW acute respiratory disease syndrome; acquired autoimmune disease syndrome;

KW AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF;

KW TL2. tumour necrosis factor-related apoptosis-inducing ligand.

XX

OS Homo sapiens.

XX

PN EP870827-A2.

XX

PD 14-OCT-1998.

XX

PF 23-DEC-1997; 97EP-00310562.

XX

PR 14-MAR-1997; 97US-0041230P.

PR 09-MAY-1997; 97US-00853684.

PR 22-AUG-1997; 97US-00916625.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Deen KC, Young PR;

XX

DR WPI; 1998-523156/45.

DR N-PSDB; AAV63096.

XX

PT DNA encoding tumour necrosis factor receptor TR6 - and corresponding

PT polypeptide, antibody, agonist, antagonist, etc.

XX

PS Disclosure; Page 32-33; 34pp; English.

XX

CC This sequence represents the human tumour necrosis factor (TNF)-related

CC receptor, TL2 (also known as tumour necrosis factor-related apoptosis-

CC inducing ligand, TRAIL). This protein is used in a method resulting in

CC the isolation of the novel human TNF related receptor, TR6. TR6

CC polypeptides and polynucleotides can be used in the treatment of chronic

CC and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g.

CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.

CC host disease, infection, stroke, ischaemia, acute respiratory disease

CC syndrome, restenosis, brain injury, (acquired autoimmune disease

CC syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative

CC disorders), atherosclerosis and Alzheimers disease

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Db 121 RVAAHITGRSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 5
AAW56760
ID AAW56760 standard; protein; 281 AA.
XX
AC AAW56760;
DT 05-AUG-1998 (first entry)
XX Human TRAIL polypeptide.
DE Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
KW cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
KW
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Domain 1. .18
FT /note= "N-terminal cytoplasmic domain"
FT Region 19. .38
FT /note= "transmembrane region"
FT Domain 39. .281
FT /note= "extracellular domain"
XX
PN US5763223-A.
XX
XX
PD 09-JUN-1998.
XX
XX 25-JUN-1996; 96US-00670354.
XX
PR 29-JUN-1995; 95US-00496632.
PR 01-NOV-1995; 95US-00548368.
XX
PA (IMMV) IMMUNEX CORP.
XX
XX Goodwin RG, Wiley SR;
PI
XX
DR WPI; 1998-347322/30.
DR N-PSDB; AAV29518.
XX
PT DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful
PT for producing recombinant polypeptides for research and therapy of
PT leukaemia, lymphoma, melanoma and viral infections.
XX
PS Claim 1; Col 33-36; 28pp; English.
XX
CC This represents a human tumour necrosis factor related apoptosis ligand
CC (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce
CC apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful
CC for producing the recombinant TRAIL polypeptides, which may be useful in
CC studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
CC (e.g. to isolate antigens for vaccine development). The polypeptides can
CC be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
CC treatment of blood or bone-marrow), or to treat viral infections
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGTCLVIFVFTVLLQSLCAVTVYVFTNELKQMDKYSKGIACFLKE 60

Db 1 MAMMEVQGGPSLGTCLVIFVFTVLLQSLCAVTVYVFTNELKQMDKYSKGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVAKQLRQLVRKMILRTSEETISTVQEKQONISPLVRGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVAKQLRQLVRKMILRTSEETISTVQEKQONISPLVRGPQ 120
QY 121 RVAAHITGRSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
Db 121 RVAAHITGRSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 6
AAW44354
ID AAW44354 standard; protein; 281 AA.
XX
AC AAW44354;
XX
DT 28-MAY-1998 (first entry)
XX Human AGP-1.
DE
XX
KW Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
KW bone resorption; haematopoietic disease.
XX
OS Homo sapiens.
XX
PN WO9746686-A2.
XX
PD 11-DEC-1997.
XX
XX 06-JUN-1997; 97WO-US009895.
XX
PR 07-JUN-1996; 96US-00660562.
XX
PA (AMGE-) AMGEN INC.
XX
PI Johnson MJ, Simonet WS, Danilenko DM;
XX
DR WPI; 1998-042194/04.
DR N-PSDB; AAV15295.
XX
PT Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -
PT useful for treating inflammation, bone resorption and haematopoietic
PT diseases.
XX
PS Claim 7; Page 36-37; 54pp; English.
XX
CC The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
CC factor (TNF)-related protein, involved in inflammation, myelopoiesis and
CC bone resorption. It has the same nucleic acid and amino acid (aa)
CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or
CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,
CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat
CC haematopoietic diseases associated with reduction in the number of bone
CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
CC by disease, injury or exposure to myelosuppressive agents. Host cells,
CC transformed with expression vectors containing AGP-1 DNA, are used to
CC produce recombinant AGP-1
XX

SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7
AAY01517
ID AAY01517 standard; peptide; 281 AA.
XX AAY01517;
AC AAY01517;
XX 27-MAY-1999 (first entry)

Protein associated with neurodegenerative and autoimmune diseases.

Neurodegenerative disease; autoimmune disease; inflammatory disease;
lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
surface receptor; TRAIL protein.

Homo sapiens.

FR2766713-A1.

05-FEB-1999.

04-AUG-1997; 97FR-00010176.

04-AUG-1997; 97FR-00010176.

(INMR) BIO MERIEUX.

Rieger F, Belliveau JF, Perron H;

WPI; 1999-156177/14.

Use of polypeptide derived from TRAIL protein for diagnosis of
degenerative disease - autoimmunity and inflammation, also useful in
prevention or treatment, and similar use of corresponding ligand and
nucleic acid.

Claim 2; Page 13; 21pp; French.

The specification describes the use a polypeptide corresponding to at
least the primary sequence of part of the present sequence to produce a
diagnostic, prophylactic or therapeutic composition useful in cases of
degenerative, autoimmune and inflammatory diseases. The polypeptides can
be used in treatment of neurodegenerative disease, lupus erythematosus,
rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
nervous system cells, antigenic and specifically recognise the surface
receptor of the TRAIL protein. The polypeptide is a marker of disease and
a therapeutic target, e.g. its apoptotic activity can be blocked with an

CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
CC receptors, inhibiting formation of natural complex
XX Sequence 281 AA;
SQ Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8

AAY27012

ID AAY27012 standard; protein; 281 AA.

XX AAY27012;

AC AAY27012;

XX 24-SEP-1999 (first entry)

Human Apo-2 ligand (Apo-2L) polypeptide.

Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;

lupus; immune-mediated glomerular nephritis; human.

Homo sapiens.

WO9936535-A1.

22-JUL-1999.

15-JAN-1999; 99WO-US001039.

15-JAN-1998; 98US-00007886.

15-APR-1998; 98US-00060533.

(GETH) GENENTECH INC.

Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;

WPI; 1999-444397/37.

N-PSDB; AAX86987.

A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
in mammalian cancer cells.

Claim 1; Fig 1A; 86pp; English.

This sequence represents a novel human cytokine, designated Apo-2 ligand
(Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
cells. This is useful for the treatment of cancer. Apo-2L can be used to
induce apoptosis for pathological conditions characterized by decreased
levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid

XX PS Claim 61; Fig 36; 226pp; English.

XX CC The present invention describes an antibody that binds to a human protein

CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;

CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;

CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer

CC activity and can be used to diagnose tumours in mammals, by detecting

CC complex formation when the antibody is contacted with test cells.

CC Increased expression of genes encoding (I) can also be detected to

CC diagnose tumours. Agents which inhibit the activity of (I), especially

CC the antibodies, or an antisense oligonucleotide which hybridises to genes

CC encoding (I), can be used to inhibit tumour growth, preferably by

CC inducing cell death. Methods from the present invention can be used to

CC identify compounds which inhibit the biological activity of (I). AAC58019

CC to AAC58102 represent PCR primers and hybridisation probes used in

CC examples from the present invention for human PRO sequences. AAC58103 to

CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and

CC protein sequences given in the exemplification of the present invention

XX CC

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQNISPLVRERGQ 120

Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQNISPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240

Db 181 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 11

AAB08545

ID AAB08545 standard; protein; 281 AA.

XX AC AAB08545;

XX DT 20-DEC-2000 (first entry)

XX DE Amino acid sequence of a human TRAIL polypeptide.

XX KW Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;

KW TNF related apoptosis-inducing ligand; tumour cell;

KW TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;

XX non-small cell lung carcinoma.

XX KW

OS Homo sapiens.

XX WO200048619-A1.

PN WO200048619-A1.

XX PD 24-AUG-2000.

XX PF 15-FEB-2000; 2000WO-US003891.

XX PR 16-FEB-1999; 99US-0120313P.

XX PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX PI Rosen GD;

XX DR WPI; 2000-558253/51.

DR N-PSDB; AAA64325.

XX PT Killing of tumor cells, e.g. solid tumors or carcinoma, comprises

PT administration of synergistic combination of diterpenoid diepoxide and

PT tumor necrosis factor related apoptosis-inducing ligand.

XX PS Disclosure; Page 23-24; 29pp; English.

XX CC The present sequence represents a human TRAIL (tumour necrosis factor

CC (TNF) related apoptosis-inducing ligand) polypeptide. The specification

CC describes a method for enhanced killing of tumour cells. The method

CC comprises contacting a susceptible tumour cell with a synergistic mixture

CC of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined

CC dosage to kill at least 50 % of the cells. This mixture is synergistic,

CC and so is active at lower doses and against otherwise resistant cell

CC lines. The method is used for killing tumour cells, especially solid

CC tumours or carcinomas (especially mammary carcinoma or non-small cell

CC lung carcinoma)

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQNISPLVRERGQ 120

Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQNISPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240

Db 181 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 12

AAB28691

ID AAB28691 standard; protein; 281 AA.

XX AC AAB28691;

XX DT 14-FEB-2001 (first entry)

XX DE Human AGP-1.

XX KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;

KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;

KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;

KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;

KW transplant rejection; cardiovascular disease; arteriosclerosis.

XX OS Homo sapiens.

XX WO200063253-A1.

PN WO200063253-A1.

XX PD 26-OCT-2000.

XX PF 24-MAR-2000; 2000WO-US008004.

XX 16-APR-1999; 99US-00293245.
XX (AMGE-) AMGEN INC.
XX Hsu H, Meng S;
XX WPI; 2000-665240/64.
DR N-PSDB; AAC67831.
XX Fusion protein of AGP-1 protein and an Fc region, used to treat
PT proliferative disorders, immune disorders, and virally-induced disorders.
PT
XX Claim 3; Fig 2; 93pp; English.
XX The present sequence is human AGP-1, a type II transmembrane protein.
CC Fusion proteins comprising an Fc immunoglobulin region fused to the N-
CC terminal portion of the AGP-1 protein have been produced. The fusion
CC proteins can be used to induce apoptosis in a tissue, and to treat
CC proliferative disorders, immune disorders, or virally-induced disorders.
CC The proliferative disorders include cancers, such as breast, prostate,
CC lung or colon cancer. The viral infections include hepatitis, and
CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion
CC proteins have increased biological activity compared to the soluble AGP-1
CC proteins used in prior art therapies
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 13
AAB50977
ID AAB50977 standard; protein; 281 AA.
XX
AC AAB50977;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO1096 protein.
XX
KW Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
XX
OS Homo sapiens.
XX
PN WO200073348-A2.
XX

PD 07-DEC-2000.
XX 30-MAY-2000; 2000WO-US014941.
PF
XX 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
XX
PA (GETH) GENENTECH INC.
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX WPI; 2001-016509/02.
DR N-PSDB; AAC91579.
XX
PT Twenty eight nucleic acids encoding PRO polypeptides which are useful for
PT treating various tumors, e.g. breast cancer, and other inflammatory,
PT angiogenic and immunological disorders.
XX
PS Claim 31; Fig 54; 188pp; English.
XX
CC The present sequence is one of twenty eight novel PRO polypeptides. The
CC PRO polypeptides and their agonists, including antibodies, peptides, and
CC small molecule agonists, may be used to treat various tumors, e.g.,
CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
CC central nervous system cancer, melanoma or leukaemia. They are also
CC useful for treating other disorders such as neuronal, glial, astrocytal,
CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
CC blastocoelec disorders, and inflammatory, angiogenic and immunological
CC disorders
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
XX

Db 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

RESULT 14
AAB67243

ID AAB67243 standard; protein; 281 AA.

XX
AC AAB67243;

DT 18-APR-2001 (first entry)

XX
DE Human Apo2 ligand.

XX
KW Human; Apo2 ligand: divalent metal ions; viral infection; cancer.

XX
OS Homo sapiens.

XX
PN WO200100832-A1.

XX
PD 04-JAN-2001.

XX
PF 26-JUN-2000; 2000WO-US017579.

XX
PR 28-JUN-1999; 99US-0141342P.

XX
PA (GETH) GENENTECH INC.

PI Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
PI O'connell M, Pai R, Shahrokh Z, Simmons L;

XX
DR WPI; 2001-123012/13.

XX
PT Use of divalent metal ions for making Apo-2 ligand and in formulations
PT containing Apo-2 ligand for increasing yield and stability of ligand
PT trimers, useful for therapeutic applications.

XX
PS Claim 6; Fig 1; 60pp; English.

XX
CC The present invention relates to a formulation comprising Apo-2 ligand
CC and divalent metal ions. Apo-2 ligand and the formulation are useful for
CC treating cancers and viral infections. Addition of divalent metal ions
CC for making Apo-2 ligand and formulations containing Apo-2 ligand results
CC in increased yield and stability of Apo-2 ligand trimers

XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60
|||||

Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60
|||||

QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQQNISPLVRERGQ 120
|||||

Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQQNISPLVRERGQ 120
|||||

QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
|||||

Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
|||||

QY 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 240
|||||

Db 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 240
|||||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

RESULT 15
AAE11031

ID AAE11031 standard; protein; 281 AA.

XX
AC AAE11031;

XX
DT 18-DEC-2001 (first entry)

XX
DE Human TNF related apoptosis inducing ligand (TRAIL) protein.

XX
KW Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
KW melanoma.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Domain 1. .18
FT /label= N_terminal_cytoplasmic_domain
FT Region 19. .38
FT /label= Transmembrane_region
FT Domain 39. .281
FT /label= Extracellular_domain

XX
PN US6284236-B1.

XX
PD 04-SEP-2001.

XX
PF 26-MAY-1999; 99US-00320424.

XX
PR 29-JUN-1995; 95US-00496632.
PR 01-NOV-1995; 95US-00548368.
PR 25-JUN-1996; 96US-00670354.
PR 26-MAR-1998; 98US-00048641.
PR 10-NOV-1998; 98US-00190046.

XX
PA (IMMV) IMMUNEX CORP.

XX
PI Wiley SR, Goodwin RG;

XX
DR WPI; 2001-595463/67.
DR N-PSDB; AAD18395.

XX
PT New tumor necrosis factor related apoptosis inducing ligand polypeptides
PT for treating viral infections (e.g. bovine viral diarrhoea or human
PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).

XX
PS Claim 2; Col 45-48; 41pp; English.

XX
CC The invention relates to a cytokine designated as tumour necrosis factor
CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
CC of certain target cells, including cancer cells and virally infected
CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
CC treating viral infections (e.g. bovine viral diarrhoea or human
CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
CC melanoma), as a research reagent useful in studying apoptosis including
CC the regulation of programmed cell death. TRAIL DNA sequences may be
CC employed in developing a gene therapy approach to treating disorders
CC mediated by defective or insufficient amounts of TRAIL, in the production
CC of TRAIL polypeptides and as probes or primers in polymerase chain
CC reactions (PCR). The present sequence is human TRAIL protein

XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60
|||||

Db 1 MAMMEVQGGPSLQGTCLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKRMILRTSEETISTVQEKQONISPLVRERGPO 120
|||||

Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKRMILRTSEETISTVQEKQONISPLVRERGPO 120
|||||

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
|||||

Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
|||||

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
|||||

Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
|||||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

RESULT 16
AAB48350
ID AAB48350 standard; protein; 281 AA.
XX
AC AAB48350;
XX
DT 20-APR-2001 (first entry)
XX
DE Human TL2 polypeptide.
XX
KW Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TL2;
KW antiinflammatory; immunosuppressive; cerebroprotective; vasotropic;
KW antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;
KW nootropic; neuroprotective; antiarthritic; antirheumatic; antiischemic;
KW gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.
XX
OS Homo sapiens.
XX
PN WO200077191-A1.
XX
PD 21-DEC-2000.
XX
PF 12-JUN-2000; 2000WO-US016134.
XX
PR 15-JUN-1999; 99US-00333593.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;
XX
FI WPI; 2001-112223/12.
DR N-PSDB; AAC84745.
XX
PT New tumor necrosis factor related receptor TR6 polynucleotides and
PT polypeptides useful for e.g. for treating chronic and acute inflammation,
PT arthritis, septicemia, autoimmune diseases, infection, cancer, bone
PT diseases.
XX
PS Disclosure; Page 26; 47pp; English.
XX
CC The invention relates to a human tumour necrosis factor (TNF) related
CC receptor, TR6. TR6 can be expressed by standard recombinant methodology.
CC The TR6 polypeptides are useful for treating chronic and acute
CC inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g.
CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
CC host disease, infection, stroke, ischaemia, acute respiratory disease
CC syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,
CC atherosclerosis, and Alzheimer's disease. These may also be used to
CC inhibit production of TNF-alpha and eicosanoids, as research reagents and
CC materials for discovering treatments and diagnostics to animal and human
CC diseases. The polypeptides may further be used as immunogens to produce
CC antibodies immunospecific for the TR6 polypeptides. The polynucleotides
CC may also be used as hybridization probes for cDNA and genomic DNA, for
CC isolating full-length cDNAs and genomic clones encoding TR6 and of other

CC genes having high sequence similarity to TR6 gene, and for chromosome
CC identification. The present sequence represents a human TL2 polypeptide.
CC TL2 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and is
CC a ligand for the TL2 polypeptide
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLQGTCLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
|||||
Db 1 MAMMEVQGGPSLQGTCLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
|||||

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKRMILRTSEETISTVQEKQONISPLVRERGPO 120
|||||

Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKRMILRTSEETISTVQEKQONISPLVRERGPO 120
|||||

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
|||||

Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
|||||

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
|||||

Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
|||||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

RESULT 17
ABB08133
ID ABB08133 standard; protein; 281 AA.
XX
AC ABB08133;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human TRAIL polypeptide.
XX
KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;
KW tuberculostatic; cytostatic; human; TRAIL.
XX
OS Homo sapiens.
XX
PN WO200236141-A2.
XX
PD 10-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US044834.
XX
PR 02-NOV-2000; 2000US-0245721P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;
PI Thomas Ek;
XX
DR WPI; 2002-500114/53.
XX
PT Treating an individual suffering from infection, e.g. inflammation,
PT chickenpox or AIDS, by administering a combination of dendritic cell
PT mobilization factor or maturation agent, T cell enhancing factor and
PT antigen-specific T cells.
XX
PS Disclosure; Page 40-42; 43pp; English.
XX
CC The invention relates to treating an individual at risk for or suffering
CC from infection with a pathogenic or opportunistic organism. The method
CC involves administering a combination of two to five agents comprising:

CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
CC or (e) activated, antigen-specific T cells. The methods are useful for
CC treating an individual at risk for or suffering from infection with a
CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
CC T. cruzi, which causes Chaga's disease). The methods are especially
CC useful for treating an individual suffering from immunosuppression by
CC enhancing a lymphocyte-mediated immune response. In particular, the
CC method is useful for treating inflammations, chickenpox, oral or genital
CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T
CC cell leukemia or T cell lymphoma. The activated antigen-presenting
CC dendritic cells are useful as a vaccine adjuvant. The present sequence
CC represents a human TRAIL polypeptide fragment
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 18
ABG31630
ID ABG31630 standard; protein; 281 AA.
XX
AC ABG31630;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human TRAIL protein.
XX
KW Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;
KW dendritic cell maturation agent; T cell enhancing factor; skin cancer;
KW antigen-specific T cell; prostate cancer; liver cancer; bone tumour;
KW brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;
KW actinic keratosis; dendritic cell maturation stimulator; cytostatic;
KW dendritic cell activator; T cell enhancer; human; TRAIL.
XX
OS Homo sapiens.
XX
PN WO200266044-A2.
XX
PD 29-AUG-2002.
XX
PF 23-OCT-2001; 2001WO-US046254.
XX
PR 24-OCT-2000; 2000US-0242868P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;
XX

DR WPI; 2002-674891/72.
XX
PT Treating an individual with tumors or cancers, e.g. liver cancer or brain
PT tumor, by administering a combination of dendritic cell populations, T
PT cell enhancing factors and activated, antigen-specific T cells.
XX
PS Disclosure; Page 41-43; 44pp; English.
XX
CC The present invention relates to a new method for treating a tumour-
CC bearing subject. The method involves administering a combination of 2 to
CC 5 agents comprising dendritic cell mobilisation factor, dendritic cell
CC maturation agent, tumour-killing agent, T cell enhancing factor or
CC activated, antigen-specific T cells. The method is useful for treating
CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver
CC cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or
CC cervical intraepithelial neoplasia. The present amino acid sequence
CC represents the human TRAIL protein that was used in the method of the
CC invention
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 19
AAU75062
ID AAU75062 standard; protein; 281 AA.
XX
AC AAU75062;
XX
DT 23-APR-2002 (first entry)
XX
DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
XX
KW TRAIL; TNF; apoptosis; tumour; death domain receptor ligand;
KW diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1; carcinoma;
KW mammary adenocarcinoma; non-small cell lung carcinoma;
KW neurological malignancy; haematological malignancy; lichen planus;
KW non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;
KW malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
KW non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
KW T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
KW discoid lupus erythematosus; human.
XX
OS Homo sapiens.
XX
PN US6329148-B1.
XX
PD 11-DEC-2001.
XX
PF 15-FEB-2000; 2000US-00505250.

XX 16-FEB-1999; 99US-0120313P.
PR 20-AUG-1999; 99US-0149989P.
XX
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX
XX Rosen GD, Kao P;
PI
XX
XX WPI; 2002-121125/16.
DR N-PSDB; ABK13192.
XX
XX Use of a synergistic combination of death domain receptor ligands and
PT diterpenoid triepoxides for killing of tumor cells.
XX
XX Disclosure; Col 17-20; 20pp; English.
XX
XX This invention relates to a novel method for enhanced killing of tumour
CC cells comprising contacting a tumour cell with a synergistic combination
CC of a death domain receptor ligand and a diterpenoid triepoxide. This
CC method has cytostatic activity and works by blocking TNF-alpha mediated
CC induction of c-IAP2 and c-IAP1. The method of the invention may be used
CC for treating tumours, particularly solid tumours, e.g. carcinoma, mammary
CC adenocarcinoma and non-small cell lung carcinoma also neurological
CC malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma,
CC chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis
CC fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-
CC cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid
CC lupus erythematosus, lichen planus. The combination may be administered
CC with other active agents, e.g. anti- metastatic, anti-tumour or anti-
CC angiogenic agents. The potent synergy between the diterpenoids and the
CC death domain ligands allows increased killing at equivalent or lower
CC doses, and can sensitise otherwise resistant cells. This sequence
CC represents the human TNF related apoptosis inducing ligand (TRAIL)
CC protein sequence. TRAIL is a death domain receptor used in the used
CC method of the invention in combination with diterpenoid triepoxides to
CC kill tumours by induction of apoptosis
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 20
AAM51077
ID AAM51077 standard; protein; 281 AA.
XX
AC AAM51077;
XX
DT 30-MAY-2002 (first entry)
XX Human Apo-2 ligand (TRAIL).

XX Apo-2 ligand; Apo-2L; TRAIL; human; apoptosis; colorectal cancer; tumour;
KW antitumour; therapy.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Protein 114..281
FT /note= "Apo-2L polypeptide used in method of Claim 18"
XX
XX WO200209755-A2.
PN
XX
XX 07-FEB-2002.
XX
XX 27-JUL-2001; 2001WO-US023691.
XX
XX 27-JUL-2000; 2000US-0221256P.
PR (GETH) GENENTECH INC.
XX
XX Escandon E, Fox JA, Kelley SK, Xiang H;
PI
XX WPI; 2002-268997/31.
XX
XX Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I
PT inhibitor class, and Apo-2 ligand receptor agonist for enhancing
PT apoptosis in mammalian cells, or for treating cancer in a mammal.
XX
XX Claim 18; Page 79-80; 84pp; English.
XX
XX The present sequence is that of human Apo-2 ligand (Apo-2L or TRAIL). The
CC invention relates to methods of inducing apoptosis in mammalian cells,
CC and especially to the use of Apo-2L receptor agonists and CPT-11 (a
CC chemotherapeutic agent of the topoisomerase I inhibitor class) to
CC synergistically induce apoptosis in mammalian cells, in particular
CC mammalian cancer cells, and especially colorectal cancer cells (claimed).
CC The cells may be in cell culture or in a mammal, e.g. a mammal suffering
CC from cancer or a condition in which induction of apoptosis in the cells
CC is desirable. A claimed method of treating cancer in a mammal comprises
CC administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is
CC administered about 6-72 hours prior to administration of the Apo-2L
CC receptor agonist. Preferred Apo-2L receptor agonists include Apo-2L
CC (especially amino acids 114-281 of the present sequence) and anti-DR4 or
CC anti-DR5 receptor antibodies. Exposure of the cancer cells to CPT-11 and
CC Apo-2L receptor agonist leads to upregulation of DR4 and DR5 receptors,
CC directing the cells towards an apoptotic pathway rather than cell cycle
CC arrest and possible DNA repair, thus providing enhanced antitumour
CC activity. An example illustrates the synergistic inhibition of tumour
CC growth by Apo-2L and CPT-11 in athymic nude mice injected s.c. with human
CC COLO205 colon carcinoma cells
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG.180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

Qy		241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEADSFFGAFLVG 281
Db		241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEADSFFGAFLVG 281

RESULT 21
ABP51954
ID ABP51954 standard; protein: 281 AA.

AC ABP51954;
XX
DT 09-OCT-2002 (first entry)

DE Human Apo-2 ligand protein sequence SEQ ID NO:4.

KW Bacterial host; protease; degP; prc; spr; anti-VEGF antibody; antibody;
 KW humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;
 KW anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;
 KW anti-CD11a; Fab'; Fab'2; Fab'2-leucine zipper fusion; anti-VEGF Fab.

OS Homo sapiens.

PN WO200248376-A2.

PD 20-JUN-2002.

07-DEC-2001: 2001WO-US047581.

PR 14-DEC-2000: 2000US-0256162P.

PA (GETH) GENENTECH INC.

Chen CY:

DR WPI; 2002-583522/62.
DR N-PSDB; ABQ73920.

Novel *Escherichia coli* strain useful for producing polypeptide, deficient in degp and prc encoding protease, and harboring mutant spr gene, product of gene suppresses growth phenotypes of strains harboring prc mutants.

PS Example 1: Fig 4: 63pp: English:

The present invention describes an *Escherichia coli* strain (I) deficient in chromosomal degp and prc encoding protease Degp and Prc, respectively, and harbouring a mutant spr gene, the product of mutant spr gene suppresses growth phenotypes exhibited by strains harbouring prc mutants. (I) is useful for producing a polypeptide, by culturing (I) comprising nucleic acid encoding the polypeptide, which is heterologous to the strain, such that the nucleic acid is expressed, and recovering the heterologous polypeptide from the strain. The heterologous polypeptide is proteolytically sensitive. Culturing of (I) is performed in a fermentor under conditions of high- or low-cell density fermentation. The polypeptide is recovered from the periplasm or culture medium of the strain. The polypeptide is an antibody (humanised or full-length antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2, anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an antibody fragment having a light chain (kappa light chain). The antibody fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18 Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence represents a human Apo-2 ligand amino acid sequence from the present invention.

Sequence 281 AA:

Query Match 100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAMMEVQGGPSLQGTCLVIVFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE	60
Db	1		60
QY	61	DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMIILRTSEETISTVQEKQQNISPLVRERGPQ	120
Db	61		120
QY	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG	180
Db	121		180
QY	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWSKDAEYGLY	240
Db	181		240
QY	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281
Db	241		281

RESULT 22

AAO19095
ID AAO19095 standard; protein; 281 AA.

AC AAO19095:

DT 22-NOV-2002 (first entry)

DE C neoformans antigen expressing dendritic cell related protein #4.

KW Human; fungicide; fungal infection; dendritic cell; antigen
KW Cryptococcus neoformans; vaccine; immunostimulant.

xx
OS
Homo sapiens.

PN WO200266053-A2

29-AUG-2002.

14-DEC-2001: 2001WO-US048288.

PR 04-JAN-2001: 2001US-0259653P.

PA (IMMV) IMMUNEX CORP.

PI Thomas EK:

DR WPI: 2002-674896/72.

Producing a population of activated, *Cryptococcus neoformans* antigen-presenting dendritic cells for preventing or treating *C. neoformans* infection comprises causing the obtained dendritic cells to present the PT antigen.

PS Disclosure: Page 29-30; 32pp; English.

The present invention relates to a method of producing a population of activated, *Cryptococcus neoformans* antigen-presenting dendritic cells, comprising causing the obtained dendritic cells to present the antigen and maturing the dendritic cells. The activated, *C. neoformans* antigen-expressing dendritic cells are useful for treating, or as vaccines or vaccine adjuvants against, *C. neoformans* infection, or for generating antigen-specific T cells. The present sequence is a human protein shown in the exemplification of the invention

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0

KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW multiple sclerosis; retinitis pigmentosa; cerebellar degeneration;
KW aplastic anaemia; myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; cancer; lupus; herpes virus infection.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Domain 15..40
FT /note= "Transmembrane domain"
FT Domain 41..281
FT /note= "Extracellular domain"
FT Modified-site 109
FT /note= "N-glycosylated"

XX
PN US6462176-B1.

XX
PD 08-OCT-2002.

XX
PF 11-SEP-1997; 97US-00928069.

XX
PR 23-SEP-1996; 96US-0026943P.

XX
PA (GETH) GENENTECH INC.

XX
PI Ashkenazi AJ;

XX
DR WPI; 2003-173840/17.
DR N-PSDB; ABX15469.

XX
PT Novel isolated Apo-3 polypeptide useful for inducing apoptosis in
PT mammalian cells, for generating antibodies, in affinity purification
PT techniques, and in competitive-type receptor binding assays.

XX
PS Example 4; Fig 4; 52pp; English.

XX
CC The invention relates to an Apo-3 polypeptide having an extracellular
CC domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide
CC has been found to stimulate or induce apoptotic activity in mammalian
CC cells. Human Apo-3 exhibits similarities to the tumour necrosis factor
CC receptor (TNFR) family of polypeptides. The invention also relates to a
CC chimeric molecule comprising an extracellular domain sequence comprising
CC residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The
CC Apo-3 polypeptide is useful therapeutically to induce apoptosis in
CC mammalian cells. Decreased levels of apoptosis has been associated with
CC conditions such as cancer, lupus, and herpes virus infection. Increased
CC levels of apoptosis are associated with diseases such as acquired
CC immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis
CC pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial
CC infarction, stroke, reperfusion injury, and toxin-induced liver disease.
CC The Apo-3 polypeptide is also useful in non-therapeutic applications such
CC as in quantitative diagnostic assays as a control against which samples
CC containing unknown quantities of Apo-3 may be prepared, in generating
CC antibodies, as standards in assays for Apo-3, in affinity purification
CC techniques, and in competitive-type receptor binding assays. The chimeric
CC molecule is useful therapeutically to inhibit apoptosis or nuclear factor
CC -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-
CC Apo-3 antibodies. The present sequence represents polypeptide sequence of
CC the human Apo-2 ligand protein which is also reported to be involved in
CC apoptotic cell death. In the current invention the apoptotic activity of
CC the Apo-2 ligand protein was measured on human lymphoid cells

XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MAMMEVQGSPLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMCKYKSGIACFLKE 60
Db 1 MAMMEVQGSPLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMCKYKSGIACFLKE 60

Oy 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

Oy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Oy 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

Oy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 25
ABU10205
ID ABU10205 standard; protein; 281 AA.
XX
AC ABU10205;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human Apo-2 ligand.
XX
KW Human; Apo-2 ligand; apoptosis; gene therapy; inflammation; cancer;
KW neurodegenerative disease; immunosuppressive; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003004313-A1.
XX
PD 02-JAN-2003.
XX
PF 28-MAR-2002; 2002US-00112193.
XX
PR 23-SEP-1996; 96US-0026943P.
PR 11-SEP-1997; 97US-00928069.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
DR WPI; 2003-438872/41.
DR N-PSDB; ACA61696.

New isolated Apo-3 polypeptides, useful for stimulating or inducing
PT apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo
PT or ex vivo gene therapy techniques.

XX
PS Example 4; Fig 4; 50pp; English.

XX
CC The invention relates to an isolated Apo-3 polypeptide. The Apo-3
CC polypeptides are useful for stimulating or inducing apoptotic activity in
CC mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy
CC techniques. The Apo-3 chimeric molecules are useful for inhibiting
CC apoptosis, or as immunogens used in generating antibodies. The
CC antagonistic antibodies may be used to block excessive apoptosis, for
CC instance in neurodegenerative disease, or to block potential autoimmune/
CC inflammatory effects of Apo-3 resulting from NF-kappaB activation. The
CC nucleic acid sequences are useful as diagnostics for tissue-specific
CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or
CC knockout animals. The transgenic or knockout animals are useful in
CC developing and screening of therapeutically useful reagents. The present
CC sequence represents the amino acid sequence of human Apo-2 ligand

XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAMMEVQGGPSLQGTCLVLI	121	99US-0115554P.
				99US-0115558P.
Db	1	MAMMEVQGGPSLQGTCLVLI	120	99US-0116533P.
				99WO-US005028.
Qy	61	DDSYNDPNDDEESMNSPCWQVKWQLRQLV	120	99US-0123618P.
				99US-00284291.
Db	61	DDSYNDPNDDEESMNSPCWQVKWQLRQLV	120	99WO-US008615.
				99US-0131294P.
Qy	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG	180	99WO-US012252.
				99US-0140650P.
Db	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG	180	99US-0141037P.
				99US-0144758P.
Qy	181	FYIYSQTYFRFQEEIKENTKNDKOMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY	240	99US-00380137.
				99US-00380138.
Db	181	FYIYSQTYFRFQEEIKENTKNDKOMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY	240	99WO-US020111.
				99WO-US020594.
Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281	99US-00380913.
				99US-00403297.
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281	99US-0162506P.
				99US-00423741.
RESULT 26				
ABU71443				
ID	ABU71443	standard; protein; 281 AA.		99WO-US028313.
AC	ABU71443;			99WO-US028634.
XX				99WO-US028551.
DT	09-JUN-2003	(first entry)		99US-0170262P.
XX				99WO-US030095.
DE	Human neoplasia inhibiting PRO polypeptide PRO1096.			99WO-US030999.
XX				2000WO-US000376.
KW	Human; tumour; cancer; neoplasia; liver cancer; sarcoma; breast cancer;			2000WO-US003565.
KW	ovarian cancer; renal cancer; colorectal cancer; melanoma;			2000WO-US004341.
KW	uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;			2000WO-US004342.
KW	gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;			2000WO-US005841.
KW	central nervous system cancer; hepatic carcinoma; glioblastoma;			2000WO-US006884.
KW	neural disorder; glial disorder; astrocytal disorder;			2000WO-US008439.
KW	hypothalamic disorder; glandular disorder; macrophagal disorder;			2000WO-US013705.
KW	epithelial disorder; stromal disorder; blastocoeic disorder;			2000WO-US014042.
XX	inflammatory disorder; angiogenic disorder; immunologic disorder.			2000WO-US014941.
OS	Homo sapiens.			2000WO-US015264.
XX				2000WO-US022031.
PN	US2002192209-A1.			2000WO-US023522.
XX				2000US-00709238.
PD	19-DEC-2002.			2000WO-US030873.
XX				2000WO-US032678.
PF	30-NOV-2001; 2001US-00001054.			2001WO-US006520.
XX				2001WO-US006566.
PR	17-SEP-1997; 97US-0059114P.			2001US-00802706.
PR	27-MAR-1998; 98US-0079689P.			2001US-00866034.
PR	30-MAR-1998; 98US-0079920P.			2001WO-US017092.
PR	24-APR-1998; 98US-0082999P.			2001US-00872034.
PR	29-APR-1998; 98US-0083545P.			2001US-00872035.
PR	12-MAY-1998; 98US-0085149P.			2001WO-US017800.
PR	02-JUN-1998; 98US-0087607P.			2001US-00882636.
PR	11-JUN-1998; 98US-0088858P.			2001WO-US019692.
PR	25-JUN-1998; 98US-0090691P.			2001WO-US021066.
PR	17-AUG-1998; 98US-0096891P.			2001WO-US021735.
PR	17-AUG-1998; 98US-0096894P.			2001US-00918585.
PR	10-SEP-1998; 98US-0099803P.			2001US-00924419.
PR	14-SEP-1998; 98WO-US018824.			2001US-00927796.
PR	15-SEP-1998; 98US-0100390P.			2001US-00929404.
PR	23-SEP-1998; 98US-0101476P.			2001US-00941992.
PR	10-NOV-1998; 98US-0107783P.			2001WO-US027099.
PR	18-NOV-1998; 98US-0108849P.			2001US-00946374.
PR	19-NOV-1998; 98US-00180997.			
PR	15-DEC-1998; 98US-0112420P.			
PR	22-DEC-1998; 98US-00218517.			
PR	22-DEC-1998; 98US-0113296P.			
PR	05-JAN-1999; 99WO-US000106.			

(GETH) GENENTECH INC.

Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
Shelton DL, Smith V, Watanabe CK, Wood WI;

WPI; 2003-328851/06.
N-PSDB; ACA58016.

Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
treating tumor, preferably cancer, or for treating neuronal, glial,

PT hypothalamic, stromal, inflammatory, angiogenic and immunologic
PT disorders.

XX
PS Claim 32; Fig 54; 186pp; English.

The invention relates to an isolated secreted and transmembrane polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its associated signal peptide or PRO polypeptide extracellular domain with or without its associated signal peptide. The PRO polypeptide or an antibody binding to it is useful for inhibiting the growth of a tumor cell. A composition containing a PRO polypeptide is useful for inhibiting neoplastic cell growth or for treating a tumour, preferably cancer (such as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder, gastric, pancreatic, vulval, thyroid, central nervous system cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or leukaemia) in a mammal. The PRO polypeptide is useful for identifying its agonists. The PRO polypeptide or an antibody binding to it is useful in the preparation of a medicament for treating a condition which is responsive to the PRO polypeptide or an antibody binding to it. The PRO polypeptide or an antibody binding to it is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelec, inflammatory, angiogenic and immunologic disorders. The present sequence represents the amino acid sequence of a PRO polypeptide of the invention

SQ Sequence 281 AA;

Query Match	100.0%;	Score 1478;	DB 6;	Length 281;
Best Local Similarity	100.0%;	Pred. No. 3.8e-137;		
Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	

Qy	1	MAMMEVQGGPSLGQTCLVLI	FTVLLQSLCVA	TVYVFTN	LKQMDKYSKSGIACFLKE	60
Db	1	MAMMEVQGGPSLGQTCLVLI	FTVLLQSLCVA	TVYVFTN	LKQMDKYSKSGIACFLKE	60
Qy	61	DDSYWDPNDEESMNSPCWQVKWQLRQLV	RKMILRTSEETIS	TVQEKQONISPLVR	RGPG	120
Db	61	DDSYWDPNDEESMNSPCWQVKWQLRQLV	RKMILRTSEETIS	TVQEKQONISPLVR	RGPG	120
Qy	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINS	WESSRSGHSFLSNHLR	NGELVIHEKG	180	
Db	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINS	WESSRSGHSFLSNHLR	NGELVIHEKG	180	
Qy	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQYI	YKYTSYPDPILL	MKSARNSCWSKDAEYGLY	240	
Db	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQYI	YKYTSYPDPILL	MKSARNSCWSKDAEYGLY	240	
Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEA	SFFGAFLVG	281		
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEA	SFFGAFLVG	281		

RESULT 27

ABG72738
ID ABG72738 standard; protein; 281 AA.

AC ABG72738;

DT. 17-FEB-2003 (first entry)

Human TNF-related apoptosis inducing ligand (TRAIL) protein.

Human; allergic disease; allergy; TNF; TRAIL; diagnosis; tumour necrosis factor-related apoptosis inducing ligand; atopic skin inflammation.

OS Homo sapiens.

PN WO200283946-A1.

PD 24-OCT-2002.

PF 01-MAR-2002; 2002WO-JP001914.

XX
PR 06-APR-2001; 2001JP-00108631.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN AGENCY NATION

PI Sugita Y, Heishi M, Kagaya S, Gunji S, Tsujimoto G;
XX
DR WPI; 2003-093037/08.
DR N-PSDB; ABX13715.

Measurement of the expression level of TNF related apoptosis inducing ligand gene for diagnosis and examination of allergic disease and screening agents for allergic disease treatment.

PS Disclosure; Page 51-52; 58pp; Japanese.

The invention discloses a method for examining allergic diseases, which comprises measuring the expression level of tumour necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL) gene in a specimen from the patient and comparing this level with the level in healthy persons. TRAIL gene expression is decreased in patients. The nucleic acids and polypeptide can be used to screen for agents for the treatment of allergic diseases, possibly using a transgenic rodent as a model animal for the disease, with effectiveness determined by changes in expression levels or protein activity. The method is useful for the diagnosis, examination, prevention and treatment of allergic diseases, including atopic skin inflammation. The sequence presented is the human TRAIL protein

Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;

QY	1	MAMMEVQGGPSLQGTCTCLIVIFTVLLQSLCAVTVYVYFTNELKQMDKYKSGIACPLKE	60
Db	1	MAMMEVQGGPSLQGTCTCLIVIFTVLLQSLCAVTVYVYFTNELKQMDKYKSGIACPLKE	60
QY	61	DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQQNISPLVRERGPQ	120
Db	61	DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQQNISPLVRERGPQ	120
QY	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG	180
Db	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG	180
QY	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSPDPILLMKSARNSCWSKDAEYGLY	240
Db	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSPDPILLMKSARNSCWSKDAEYGLY	240
QY	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281

RESULT 28

AAO29543
ID AAO29543 standard; protein; 281 AA.

AC AAO29543;

DT 27-AUG-2003 (first entry)

Human TRAIL protein.

KW Human; TNF-related apoptosis-inducing ligand; Kaposi's sarcoma; cancer;
KW hyperproliferative disorder; rheumatoid arthritis; Parkinson's disease;
KW neurodegenerative disorder; Alzheimer's disease; Hashimoto's disease;
KW allergic disorder; acquired immune deficiency syndrome; ocular disorder;
KW myasthenia gravis; autoimmune disorder; Huntington's disease; vaccine;
KW septic shock; multiple sclerosis; inflammatory disorder; liver injury;

PF 01-MAR-2002; 2002WO-JP001914.

The antibody is useful for treating disorders mediated or exacerbated by TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic thrombocytopaenic purpura (TTP), adult haemolytic uraemic syndrome (HUS) (even though it can strike children as well) small blood vessel clotting disorders e.g., cardiac problems in paediatric AIDS patients and systemic lupus erythematosus (SLE). The present sequence represents human TRAIL Sequence 281 AA;

of tumour necrosis factor (TNF) ligand family members, and their use in the detection, prevention and treatment of disease. In one embodiment, the heterotrimeric complex comprises full-length or extracellular portions of TRAIL and full-length or extracellular portions of other TNF ligand family members, preferably RANKL. The heterotrimeric complexes of the invention are useful for treating an autoimmune disease, cancer or osteoporosis, and particularly for inhibiting cancer cell proliferation, increased B cell proliferation, or inducing apoptosis of T cells. A claimed method of inducing apoptosis of T cells comprises administering a heterotrimeric complex consisting of FasL and LIGHT, TNF-alpha, lymphotoxin-beta or TRAIL. A claimed method of inhibiting cancer cell proliferation involves administering a heterotrimeric complex consisting of TRAIL and CD40L or RANK. A claimed method of treating osteoporosis comprises administering an antibody against a complex comprising RANKL and TRAIL.

XX	PI	Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;
SQ	XX	WPI; 2003-140454/13.
	XX	Novel antibody useful for treating cancers and other hyperproliferative disorders, immunospecifically binds to TRAIL receptor and comprises variable heavy or light chain complementarity determining regions.
	XX	Disclosure; Page 300-301; 301pp; English.
	CC	The present invention relates to novel antibodies that immunospecifically bind to TRAIL receptor (TR4). Sequences of the invention are useful for treating, preventing or ameliorating cancer (e.g. colon, breast, uterine, pancreatic, lung, gastrointestinal or central nervous system cancer e.g. medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in human. They are useful for detecting expression of TR4 polypeptide and detecting, diagnosing, prognosing or monitoring cancers and other hyperproliferative disorders. Antibodies of the invention are useful for treating, preventing or ameliorating neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, cerebellar degeneration and Huntington's disease), immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis, Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease, polyomyositis, immune-related glomerulonephritis, myasthenia gravis, Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory disorders (e.g. asthma, allergic disorders and rheumatoid arthritis), infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS), herpes viral infections and other viral infections) and proliferative disorders. They are also useful for treating myelodysplastic syndromes (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke, myocardial infarction and reperfusion injury), septic shock, cachexia, anorexia and toxin-induced liver diseases (such as alcohol). They are also useful for treating cardiovascular disorders including peripheral artery diseases such as limb ischaemia, arrhythmia, congestive heart failure and cardiovascular tuberculosi, diseases or disorders associated with neovascularisation and ocular disorders, for wound healing, for promoting angiogenesis and as adjuvants to enhance immune responsiveness to specific antigen e.g. viral antigen. They are also useful in the preparation or recovery from surgery, trauma, radiation therapy and transplantation. The present sequence is human TR4 ligand, TRAIL protein used in the invention
	XX	Sequence 281 AA;
	SQ	
		Query Match 100.0%; Score 1478; DB 6; Length 281;
		Best Local Similarity 100.0%; Pred. No. 3.8e-137;
		Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0
	QY	1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
	Db	1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
	QY	61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120
	Db	61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120
	QY	121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHE 180
	Db	121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHE 180
	QY	181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKTSYPDPILLMKSARNSCWSKDAEYGL 240
	Db	181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKTSYPDPILLMKSARNSCWSKDAEYGL 240
	QY	241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
	Db	241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
		RESULT 34
	ID	AAO31151
	XX	AAO31151 standard; protein; 281 AA.

QY	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIHEKG	181
Db	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIHEKG	180
QY	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY	240
Db	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY	240
QY	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281
RESULT 36			
ID	ADB61471		
ID	ADB61471 standard; protein; 281 AA.		
XX			
AC	ADB61471;		
XX			
DT	04-DEC-2003 (first entry)		
XX			
DE	Native human Apo-2 ligand protein.		
XX			
KW	Apo-2 ligand; DR5.Apo2L complex; receptor contact region;		
KW	high solvent accessibility; cytostatic; antiarthritic; neuroprotective;		
KW	trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;		
KW	lung; breast; immune-related disease; arthritis; multiple sclerosis;		
KW	native; human.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003029420-A2.		
XX			
PD	10-APR-2003.		
XX			
PF	01-OCT-2002; 2002WO-US031210.		
XX			
PR	02-OCT-2001; 2001US-0326622P.		
XX			
PA	(GETH) GENENTECH INC.		
XX			
PI	Kelley RF, Lindstrom SH;		
XX			
DR	WPI; 2003-541400/51.		
DR	N-PSDB; ADB61470.		
XX			
PT	Novel isolated Apo-2 ligand variant polypeptide useful for treating		
PT	cancer or an immune-related disease such as multiple sclerosis, comprises		
XX	amino acid substitutions in the native sequence of the Apo-2 ligand.		
PS	Claim 1; Fig 1; 92pp; English.		
XX			
CC	The invention relates to a novel isolated Apo-2 ligand variant		
CC	polypeptide having a sequence that differs from the native sequence		
CC	having 281 amino acids given in specification. The Apo-2 ligand variant		
CC	polypeptide is selected from a polypeptide having substitutions at		
CC	residue positions identified from x-ray crystal structure of the		
CC	DR5.Apo2L complex. The polypeptide having the substitutions made at		
CC	residue position(s) selected from 20 positions such as S96C, S101C,		
CC	S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,		
CC	R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the		
CC	residue position is, outside of the receptor contact region of the		
CC	DR5.Apo2L complex, and displays high solvent accessibility in the crystal		
CC	structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide		
CC	and further compositions have the following activities: cytostatic,		
CC	antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,		
CC	an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for		
CC	inducing apoptosis in mammalian cells, by exposing mammalian cells		
CC	expressing a receptor selected from DR4 receptor and DR5 receptor to a		
CC	therapeutically effective amount of the Apo-2 ligand variant polypeptide,		
CC	Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are		
CC	colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,		

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CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
CC immune-related disease (such as arthritis or multiple sclerosis) in a
CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the native human Apo-2 ligand protein of
CC the invention.
XX
SQ Sequence 281 AA;

Query Match          100.0%; Score 1478; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVFTNELKQMDKYKSGIACFLKE 60
   |||||||
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVFTNELKQMDKYKSGIACFLKE 60
   |||||||

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQQNISPLVRERGPQ 120
   |||||||
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQQNISPLVRERGPQ 120
   |||||||

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
   |||||||
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
   |||||||

QY 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSKDAEYGLY 240
   |||||||
Db 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSKDAEYGLY 240
   |||||||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
   |||||||
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
   |||||||

```

RESULT 37
ADC35202
ID ADC35202 standard; protein; 281 AA.
XX
XX AC ADC35202;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human TNF ligand family member #10.
XX
KW human; tumour necrosis factor; TNF ligand; endokine alpha;
KW excessive bone resorption disorder; osteoporosis; Paget's disease;
XX arterial calcification.
XX
OS Homo sapiens.
XX
PN US2003100074-A1.
XX
PD 29-MAY-2003.
XX
PF 15-AUG-2002; 2002US-00218547.
XX
PR 16-AUG-2001; 2001US-0312542P.
PR 30-OCT-2001; 2001US-0330761P.
XX
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (NARD/) NARDELLI B.
XX
PI Yu G, Ni J, Rosen CA, Nardelli B;
XX
DR WPI; 2003-696072/66.
DR N-PSDB; ADC35201.
XX
PT New Endokine alpha gene useful for preparing a composition for tre
PT disease associated with excessive or insufficient bone resorption
PT osteoporosis, Paget's disease or arterial calcification.

XX Disclosure; SEQ ID NO 20; 145pp; English.

PS The invention relates to an isolated nucleic acid molecule encoding a

XX tumour necrosis factor family ligand. A composition comprising the

CC isolated antibody or its fragment is used for treating an individual in

CC need of decreased level of endokine alpha activity. The endokine alpha

CC polypeptide present in a heterotrimeric complex is used for treating an

CC individual having a disorder associated with excessive bone resorption,

CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an

CC individual having a disorder associated with insufficient bone resorption

CC comprises administering an endokine alpha antagonist, which is the

CC antibody that binds specifically to endokine alpha polypeptide. The

CC present sequence represents the amino acid sequence of a tumour necrosis

CC factor family ligand.

XX

SEQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 7; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVREGPQ 120

Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVREGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

Db 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

XX New polynucleotides and polypeptides for predicting the activity of

PT compounds that interact with protein tyrosine kinases and/or protein

PT tyrosine kinase pathways.

XX Claim 10; SEQ ID NO 269; 139pp; English.

PS The present invention describes a predictor set comprising a plurality of

XX polynucleotides or polypeptides whose expression pattern is predictive of

CC the response of cells to treatment with a compound that modulates protein

CC tyrosine kinase activity or members of the protein tyrosine kinase

CC pathway. Also described: (1) predicting whether a compound is capable of

CC modulating the activity of cells, comprising obtaining a sample of cells,

CC determining whether the cells express a plurality of markers, and

CC correlating the expression of the markers to the compound's ability to

CC modulate the activity of the cells; (2) a plurality of cell lines for

CC identifying polynucleotides and polypeptides whose expression levels

CC correlate with compound sensitivity or resistance of cells associated

CC with a disease state; and (3) identifying polynucleotides and

CC polypeptides that predict compound sensitivity or resistance of cells

CC associated with a disease state, comprising subjecting the plurality of

CC cell lines to one or more compounds, analysing the expression pattern of

CC a microarray of polynucleotides or polypeptides, and selecting

CC polynucleotides or polypeptides that predict the sensitivity or

CC resistance of cells associated with a disease state by using the

CC expression pattern of the microarray. The polynucleotides and

CC polypeptides have cytostatic activities, and can be used in gene therapy.

CC The polynucleotides and polypeptides are useful in predicting the

CC activity of compounds that interact with protein tyrosine kinases and/or

CC protein tyrosine kinase pathways. These may be used in determining drug

CC sensitivity in patients to allow the development of individualized

CC genetic profiles which aid in treating diseases and disorders (e.g.

CC cancer) based on patient response at a molecular level. The present

CC sequence is used in the exemplification of the present invention.

XX

SEQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 7; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVREGPQ 120

Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVREGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

Db 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 39

ADD19010

ID ADD19010 standard; protein; 281 AA.

XX

AC ADD19010;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human disease related protein SeqID499.

XX

KW human; disease state; cytostatic; antiinflammatory; ophthalmological;

KW antiarteriosclerotic; vulnery; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transportation; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing.

RESULT 40
ABW02276
ID ABW02276 standard; protein; 281 AA.
XX
AC ABW02276;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human TRAIL protein.
XX
KW Gastrointestinal tract disorder; tumour necrosis factor; TNF; DR3; TR6;
KW TNF-gamma-beta protein; inflammatory bowel disease; Crohn's disease;
KW ulcerative colitis; TRAIL; human.
XX
OS Homo sapiens.
XX
PN US2003198640-A1.
XX
PD 23-OCT-2003.
XX
PF 06-DEC-2002; 2002US-00310793.
XX
PR 07-NOV-1994; 94WO-US012880.
PR 05-JUN-1995; 95US-00461246.
PR 09-JAN-1998; 98US-00005020.
PR 09-FEB-1998; 98US-0074047P.
PR 07-AUG-1998; 98US-00131237.
PR 08-FEB-1999; 99US-00246129.
PR 30-APR-1999; 99US-0131963P.
PR 03-MAY-1999; 99US-0132227P.
PR 13-MAY-1999; 99US-0134067P.
PR 08-FEB-2000; 2000US-0180908P.
PR 27-APR-2000; 2000US-00559290.
PR 07-JUL-2000; 2000US-0216879P.
PR 26-MAR-2001; 2001US-0278449P.
PR 06-JUL-2001; 2001US-00899059.
PR 24-AUG-2001; 2001US-0314381P.
PR 07-DEC-2001; 2001US-0336695P.
PR 23-AUG-2002; 2002US-00226294.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Yu G, Ni J, Rosen CA, Zhang J, Wei P;
XX
DR WPI; 2003-852773/79.
DR N-PSDB; AAD63912.
XX
PT Use of tumor necrosis factor gamma-beta antagonists for treating or
PT ameliorating a disease or disorders of the gastrointestinal tract, e.g.
PT inflammatory bowel disease, Crohn's disease or ulcerative colitis.
XX
PS Disclosure; Page 140-141; Opp; English.
XX
CC The invention relates to methods and compositions for treating or
CC ameliorating a disease or disorder of the gastrointestinal tract. The
CC method involves administering a composition comprising tumour necrosis
CC factor (TNF)-gamma-beta and its receptors DR3 and TR6 to a person with,
CC or suspected of having the disease or disorder. The antagonist of TNF-
CC gamma-beta is useful for treating or ameliorating a gastrointestinal
CC tract disease or disorder, specifically an inflammatory bowel disease,
CC e.g. Crohn's disease or ulcerative colitis. The present sequence is human
CC TRAIL protein. This sequence is used to illustrate the method of the
CC invention
SQ Sequence 281 AA;

Db	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSRNSCWSKDAEYGLY	240
Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281

Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Qy 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 41
ADE76953
ID ADE76953 standard; protein; 281 AA.
XX
AC ADE76953;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human protein expressed in a liver disorder #32.
XX
KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
KW tumour; liver; inflammatory disorder; immune response disorder;
KW high-throughput screening; differential gene expression; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003108871-A1.
XX
PD 12-JUN-2003.
XX
PF 30-JUL-2001; 2001US-00919039.
XX
PR 28-JUL-2000; 2000US-0222113P.
XX
PA (KASE/) KASER M R.
XX
XX Kaser MR;
PI
XX
XX WPI; 2004-031227/03.
DR N-PSDB; ADE76952.
XX

Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver disorders.
XX
PS Claim 1; SEQ ID NO 118; 41pp; English.
XX
CC The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the

CC efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a liver disorder.
CC
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Qy 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 42
ADK72311
ID ADK72311 standard; protein; 281 AA.
XX
AC ADK72311;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human Apo-2 ligand with potential substitutions highlighted #4.
XX
KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand; variant; cancer; immune system disease; arthritis; multiple sclerosis; human.
KW
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 189 /note= "wild-type Tyr may be substituted by Ala, Ser or Xaa (where Xaa is encoded by an amber codon) at this location in the variant referred to in claim 17"
FT Misc-difference 191 /note= "wild-type Arg may be substituted by Lys at this location in the variant referred to in claim 17"
FT Misc-difference 193 /note= "wild-type Gln may be substituted by Arg at this location in the variant referred to in claim 17"
FT Misc-difference 264 /note= "wild-type His may be substituted by Arg, Asp, Asn, Ala, Pro or Thr at this location in the variant referred to in claim 17"
FT Misc-difference 266 /note= "wild-type Ile may be substituted by Val or Leu at this location in the variant referred to in claim 17"
FT Misc-difference 267 /note= "wild-type Asp may be substituted by Asn, Glu or Gln at this location in the variant referred to in claim 17"
XX WO2004001009-A2.
PN
XX 31-DEC-2003.
PD

XX 23-JUN-2003; 2003WO-US019750.
PF
XX
PR 24-JUN-2002; 2002US-0391050P.
XX
XX (GETH) GENENTECH INC.
PA
XX Hymowitz S, Kelley RF, Lindstrom SH;
PI
XX WPI; 2004-082490/08.
DR
XX
PT New Apo-2 ligand variant polypeptide, useful for preparing a composition
PT for treating cancer or immune-related disease, e.g., arthritis or
PT multiple sclerosis.
XX
PS Claim 17; SEQ ID NO 1; 111pp; English.
XX
XX The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide, comprising a sequence that differs from the native sequence
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having
CC one or more following amino acid substitutions at the residue positions
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
CC variant polypeptide. Further disclosed are a composition comprising the
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant
CC polypeptide is useful for preparing a composition for treating cancer or
CC immune-related disease, e.g., arthritis or multiple sclerosis. The
CC current sequence represents the human Apo-2 ligand amino acid sequence.
CC Note: The variant sequence that is referred to in claim 17 may contain
CC one or more of the potential substitutions highlighted in the features
CC table for this record.
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 43
ADK72303
ID ADK72303 standard; protein; 281 AA.
XX
AC ADK72303;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human Apo-2 ligand with potential substitutions highlighted #1.
XX
KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;
KW human.

XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 96 /note= "wild-type ser may be substituted for Cys at this
FT location in the variant referred to in claim 1"
FT Misc-difference 101 /note= "wild-type ser may be substituted for Cys at this
FT location in the variant referred to in claim 1"
FT Misc-difference 111 /note= "wild-type ser may be substituted for Cys at this
FT location in the variant referred to in claim 1"
FT Misc-difference 170 /note= "wild-type Arg may be substituted for Cys at this
FT location in the variant referred to in claim 1"
FT Misc-difference 179 /note= "wild-type Lys may be substituted for Cys at this
FT location in the variant referred to in claim 1"
XX WO2004001009-A2.
PN 31-DEC-2003.
XX 23-JUN-2003; 2003WO-US019750.
PF 24-JUN-2002; 2002US-0391050P.
PR (GETH) GENENTECH INC.
XX Hymowitz S, Kelley RF, Lindstrom SH;
PI WPI; 2004-082490/08.
XX
DR New Apo-2 ligand variant polypeptide, useful for preparing a composition
XX for treating cancer or immune-related disease, e.g., arthritis or
XX multiple sclerosis.
PS Claim 1; SEQ ID NO 1; 111pp; English.
XX
XX The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide, comprising a sequence that differs from the native sequence
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having
CC one or more following amino acid substitutions at the residue positions
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
CC variant polypeptide. Further disclosed are a composition comprising the
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant
CC polypeptide is useful for preparing a composition for treating cancer or
CC immune-related disease, e.g., arthritis or multiple sclerosis. The
CC current sequence represents the human Apo-2 ligand amino acid sequence.
CC Note: The variant sequence that is referred to in claim 1 may contain one
CC or more of the potential substitutions highlighted in the features table
CC for this record.
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

XX The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide, comprising a sequence that differs from the native sequence
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having
CC one or more following amino acid substitutions at the residue positions
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
CC variant polypeptide. Further disclosed are a composition comprising the
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant
CC polypeptide is useful for preparing a composition for treating cancer or
CC immune-related disease, e.g., arthritis or multiple sclerosis. The
CC current sequence represents the wild-type human Apo-2 ligand amino acid
CC sequence.
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

RESULT 46
ADK72310
ID ADK72310 standard; protein; 281 AA.
XX
AC ADK72310;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human Apo-2 ligand with potential substitutions highlighted #3.
XX
KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;
KW human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 189
FT /note= "wild-type Tyr may be substituted by Ala, Ser, Gln
FT or Gly at this location in the variant referred to in
FT claim 10"
FT
FT Misc-difference 191
FT /note= "wild-type Arg may be substituted by Lys or Arg at
FT this location in the variant referred to in claim 10"
FT
FT Misc-difference 193
FT /note= "wild-type Gln may be substituted by Lys, Arg or
FT Thr at this location in the variant referred to in claim
FT 10"
FT
FT Misc-difference 264
FT /note= "wild-type His may be substituted by Ala, His,
FT Gly, Gln, Asp, Arg, Pro, Ser, Glu, Asn or Lys at this

FT location in the variant referred to in claim 10"
FT Misc-difference 266
FT /note= "wild-type Ile may be substituted by Leu, Met or
FT Val at this location in the variant referred to in claim
FT 10"
FT Misc-difference 267
FT /note= "wild-type Asp may be substituted by Ser, Glu,
FT Gln, Asp or Asn at this location in the variant referred
FT to in claim 10"
FT Misc-difference 269
FT /note= "wild-type Asp may be substituted by Ser, Asn,
FT Asp, Ala, Arg or Glu at this location in the variant
FT referred to in claim 10"
XX
PN WO2004001009-A2.
XX
PD 31-DEC-2003.
XX
PF 23-JUN-2003; 2003WO-US019750.
XX
PR 24-JUN-2002; 2002US-0391050P.
XX (GETH) GENENTECH INC.
PI Hymowitz S, Kelley RF, Lindstrom SH;
XX WPI; 2004-082490/08.
DR
XX
PT New Apo-2 ligand variant polypeptide, useful for preparing a composition
PT for treating cancer or immune-related disease, e.g., arthritis or
PT multiple sclerosis.
XX
PS Claim 10; SEQ ID NO 1; 111pp; English.
XX
CC The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide, comprising a sequence that differs from the native sequence
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having
CC one or more following amino acid substitutions at the residue positions
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
CC variant polypeptide. Further disclosed are a composition comprising the
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant
CC polypeptide is useful for preparing a composition for treating cancer or
CC immune-related disease, e.g., arthritis or multiple sclerosis. The
CC current sequence represents the human Apo-2 ligand amino acid sequence.
CC Note: The variant sequence that is referred to in claim 10 may contain
CC one or more of the potential substitutions highlighted in the features
CC table for this record.
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 47
ADJ63976
ID ADJ63976 standard; protein; 281 AA.
XX
AC ADJ63976;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human apoptosis inducing molecule 1, AIM-1.
XX
KW Human; apoptosis inducing molecule 1; AIM-1; apoptosis;
KW autoimmune disease; graft versus host disease; lymphadenopathy;
KW immunosuppressive; vasotropic; cytostatic; peripheral tolerance;
KW cell activation; cell proliferation; immune regulation;
KW inflammatory response; systemic lupus erythematosus;
KW immunoproliferative disease; neoplasm; tumour; restenosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..38
FT /note= "Signal peptide"
FT Protein 39..281
FT /label= Mature AIM_1
FT /note= "Claimed in claim 1"
XX
US2004038347-A1.
XX
PD 26-FEB-2004.
XX
PF 16-SEP-2003; 2003US-00662429.
XX
PR 14-MAR-1996; 96US-0013405P.
PR 13-MAR-1997; 97US-00816981.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM;
XX
WPI; 2004-203230/19.
DR N-PSDB; ADJ63975.
XX
PT Novel apoptosis inducing molecule polypeptide that induces apoptosis of
PT cell line derived from pathological tissue and induces apoptosis of T
PT cells, useful for treating lymphadenopathy, autoimmune diseases and graft
PT versus host disease.
XX
PS Claim 1; SEQ ID NO 2; 36pp; English.
XX
CC The invention relates to apoptosis inducing molecule-I protein (AIM-I)
CC comprising sequence that is 70 % identical to ADJ63976 or its mature form
CC where the polypeptide binds antibody specific to AIM-1, induces apoptosis
CC of cell line derived from pathological tissue and induces apoptosis of T
CC cells. Also included are a composition comprising AIM-1 and a carrier,
CC AIM-1 produced by a process involving expressing in a host cell a nucleic
CC acid that encodes the protein so as to produce the protein (where the
CC nucleic acid is chosen from a polynucleotide encoding AIM-1, mature AIM-
CC 1, mature/AIM-1 except for 1-5 or 5-10 conservative amino acid
CC substitutions, the amino acid sequence encoded by human cDNA contained in
CC ATCC Deposit No. 97448, and a polynucleotide that is complementary to
CC polynucleotide which hybridises at 60degreesC in a hybridisation buffer
CC consisting of 0.5 X SSC (Saline-Sodium Citrate) and 0.1 % sodium dodecyl
CC sulphate (SDS) to a polynucleotide chosen from polynucleotide encoding
CC mature/AIM 1, and a polynucleotide encoding amino acid sequence encoded
CC by human cDNA contained in ATCC Deposit No. 97448, where the
CC polynucleotide encodes a polypeptide that has the same biological
CC activity as described above). AIM-1 is useful for treating
CC lymphadenopathy, autoimmune diseases, graft versus host disease, for
CC stimulating peripheral tolerance, destroying pathologic transformed cell

CC lines, mediating cell activation and proliferation. AIM-1 proteins are
CC functionally linked as primary mediators of immune regulation and
CC inflammatory response, are useful for diagnosis and treatment of
CC disorders of cells, tissues and organisms. AIM-1 is useful as research
CC tool in elucidating biology of autoimmune disorders including systemic
CC lupus erythematosus, immunoproliferative disease lymphadenopathy and is
CC useful for inhibiting neoplasia such as tumour cell growth. AIM-1 is also
CC useful to treat diseases which required growth promotion activity e.g.,
CC restenosis. AIM-1 is useful for assessing AIM-I binding capacity of its
CC binding molecules such as receptor molecules. The present sequence
CC represents AIM-1.
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPG 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 48
ADL71816
ID ADL71816 standard; protein; 281 AA.
XX
AC ADL71816;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human apoptosis inducing molecule-I (AIM-I) protein.
XX
KW Apoptosis inducing molecule-I; AIM-I; cell activation;
KW cell differentiation; apoptosis; autoimmune disease;
KW graft-versus-host disease; lymphadenopathy; gene therapy; human.
XX
OS Homo sapiens.
XX
PN US2004047864-A1.
XX
PD 11-MAR-2004.
XX
PF 16-SEP-2003; 2003US-00662431.
XX
PR 14-MAR-1996; 96US-0013405P.
PR 13-MAR-1997; 97US-00816981.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM;
XX
DR WPI; 2004-226168/21.
DR N-PSDB; ADL71815.
XX
PT New antibodies specific to apoptosis inducing molecule I polypeptides
PT useful in research, biological, diagnostic, clinical or therapeutic

PT applications, such as in the treatment of autoimmune diseases or graft-versus-host disease.

XX Claim 1; SEQ ID NO 2; 36pp; English.

CC The invention relates to antibodies specific to apoptosis inducing molecule-I (AIM-I) polypeptides. The invention is useful in research, CC biological, diagnostic, clinical or therapeutic applications. It is also CC used for modulating activation and differentiation of cells, both CC normally and in disease states, or for mediating apoptosis and preventing CC or treating autoimmune diseases, graft-versus-host disease or CC lymphadenopathy. The invention is also useful in gene therapy. The CC present sequence is human AIM-I protein.

XX Sequence 281 AA;

SQ

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAITYVYFTNELKQMDKYSGIACFLKE 60
|||||

Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAITYVYFTNELKQMDKYSGIACFLKE 60
|||||

QY 61 DDSYWDPNDESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPO 120
|||||

Db 61 DDSYWDPNDESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPO 120
|||||

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
|||||

Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
|||||

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
|||||

Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
|||||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

RESULT 49

ADK15498

ID ADK15498 standard; protein; 281 AA.

XX AC ADK15498;

XX

DT 03-JUN-2004 (first entry)

XX Human TRAIL protein.

DE

XX Human; TRAIL; TNF related apoptosis inducing ligand; apoptosis; KW cytostatic; virucide; tumour necrosis factor; Jurkat cell; cancer; KW programmed cell death; leukaemia; colorectal cancer; viral infection; KW vaccine.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .18 /note= "Cytoplasmic domain"

FT Domain 19. .38 /note= "Transmembrane domain"

FT Domain 39. .281 /note= "Extracellular domain claimed in claim 4"

FT Region 95. .281 /note= "Claimed in claim 7"

FT

XX US2004052788-A1.

PN

XX 18-MAR-2004.

XX

PF 02-SEP-2003; 2003US-00652244.

XX 29-JUN-1995; 95US-00496632.

PR 01-NOV-1995; 95US-00548368.

PR 25-JUN-1996; 96US-00670354.

PR 26-MAR-1998; 98US-00048641.

PR 10-NOV-1998; 98US-00190046.

PR 26-MAY-1999; 99US-00320424.

PR 27-FEB-2001; 2001US-00796581.

XX (IMMV) IMMUNEX CORP.

PA

XX Willey SR, Goodwin RG;

PI

XX WPI; 2004-238577/22.

DR N-PSDB; ADK15497.

DR

XX

PT New tumor necrosis factor related apoptosis inducing ligand polypeptides, useful in studies of apoptosis, in regulating programmed cell death, or for treating leukemia, cancer (e.g. colorectal cancer) or viral infections.

PT

XX Claim 2; SEQ ID NO 2; 42pp; English.

XX

CC The invention relates to a new purified tumour necrosis factor related apoptosis inducing ligand (TRAIL) polypeptide comprising an amino acid sequence that is at least 90% identical to human TRAIL (ADK15498) or mouse TRAIL (ADK15502). The TRAIL polypeptide induces apoptosis of Jurkat cells. Also included are a purified human TRAIL polypeptide encoded by the cDNA insert of the recombinant vector deposited in strain ATCC 69849 (or a fragment of human TRAIL protein of SEQ ID NO: 2 that induces apoptosis of Jurkat cells), a fusion protein comprising a leucine zipper peptide and a soluble TRAIL polypeptide (comprising the extracellular domain) and a leucine zipper comprising ADK15510-ADK15513, an oligomer comprising at least two soluble TRAIL polypeptides (or at least two fusion proteins defined above), an antibody that specifically binds a TRAIL protein above and a method of inducing death of cancer cells (by contacting TRAIL-sensitive cancer cells with a TRAIL polypeptide or with an oligomer defined above). The TRAIL polypeptide is useful in studies of apoptosis, in regulating programmed cell death, for treating leukaemia, cancer (e.g. colorectal cancer) or viral infections, or in purifying leukaemic cells or a desired cell surface antigen which can be used in vaccine development. The TRAIL polypeptide may also be used in developing treatments for any disorder mediated by defective or insufficient amounts of TRAIL. The present sequence represents human TRAIL.

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAITYVYFTNELKQMDKYSGIACFLKE 60
|||||

Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAITYVYFTNELKQMDKYSGIACFLKE 60
|||||

QY 61 DDSYWDPNDESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPO 120
|||||

Db 61 DDSYWDPNDESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPO 120
|||||

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
|||||

Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
|||||

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
|||||

Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
|||||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

RESULT 50

ADN07587
ID ADN07587 standard; protein; 281 AA.
XX
AC ADN07587;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human apoptosis inducing molecule-1 protein.
XX
KW Apoptosis inducing molecule I; AIM-I; therapeutic; autoimmune disorder;
KW systemic lupus erythematosus;
KW immunoproliferative disease lymphadenopathy; IPL;
KW angioimmunoproliferative lymphadenopathy; AIL; rheumatoid arthritis;
KW diabetes; multiple sclerosis; graft versus host disease;
KW lymphoproliferative disease; lymphadenopathy; neoplasia;
KW tumour cell growth; restenosis; haematopoiesis;
KW chromosome identification; pancreatic tumour; endometrial tumour;
KW T-cell lymphoma; gene therapy; human.
XX
OS Homo sapiens.
XX
PN US2004048340-A1.
XX
PD 11-MAR-2004.
XX
PF 16-SEP-2003; 2003US-00662430.
XX
PR 14-MAR-1996; 96US-0013405P.
PR 13-MAR-1997; 97US-00816981.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM;
XX
DR WPI; 2004-238497/22.
DR N-PSDB; ADN07586.
XX
PT Novel human apoptosis inducing molecule I useful for treating
PT lymphadenopathy, systemic lupus erythematosus, rheumatoid arthritis and
PT multiple sclerosis.
XX
PS Claim 1; SEQ ID NO 2; 35pp; English.
XX
CC The present invention relates to apoptosis inducing molecule I (AIM-I)
CC polypeptide and the encoding polynucleotide useful in biological,
CC diagnostic, clinical and therapeutic arts. The invention is useful in
CC treating autoimmune disorders such as systemic lupus erythematosus,
CC immunoproliferative disease lymphadenopathy (IPL),
CC angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
CC diabetes and multiple sclerosis, graft versus host disease,
CC lymphoproliferative disease such as lymphadenopathy, in inhibiting
CC neoplasia such as tumour cell growth, in treating restenosis and
CC regulating haematopoiesis in endothelial cell development. The invention
CC is useful in chromosome identification and as a diagnostic marker for
CC determining expression of AIM-I polypeptide in tumour cell lines
CC including pancreatic tumour, endometrial tumour and T-cell lymphoma. The
CC invention is also useful in gene therapy. The present sequence is human
CC apoptosis inducing molecule I (AIM-I) protein.
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGTCLVIFTVLLQSLCAVTVYVFTNELKMQDKYSGIACFLKE 60
Db |||||
1 MAMMEVQGGPSLGTCLVIFTVLLQSLCAVTVYVFTNELKMQDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120
Db |||||
61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIHEKG 180
Db |||||
121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db |||||
181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db |||||
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 51
ADN14209
ID ADR14209 standard; protein; 281 AA.
XX
AC ADR14209;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human NF-kappaB pathway-associated protein SeqID210.
XX
KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW immunosuppressive; vulnery; gene therapy; immune disorder;
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW viral replication; host cell survival; evasion of immune response;
KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW autoimmune disorder; hyper immune activity;
KW aberrant acute phase response; hypercongenital condition; birth defect;
KW necrotic lesion; wound; organ transplant rejection;
KW aberrant signal transduction; proliferating disorder; cancer;
KW HIV propagation; human.
XX
OS Homo sapiens.
XX
PN WO2004065577-A2.
XX
PD 05-AUG-2004.
XX
PF 13-JAN-2004; 2004WO-US000798.
XX
PR 14-JAN-2003; 2003US-0440068P.
PR 12-MAY-2003; 2003US-0469757P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Nadler SG, Neubauer MG, Feder JN, Carman J;
XX
XX WPI; 2004-562168/54.
DR N-PSDB; ADR14208.
XX
PT New isolated polynucleotides and polypeptides associated with NF-kappaB
PT pathway, useful for diagnosing, treating, or preventing disorders or
PT diseases associated with NF-kappaB pathway.
XX
PS Claim 6; SEQ ID NO 210; 237pp; English.
XX
CC This invention relates to the novel association of protein sequences (and
CC the genes which encode them) to the NF-kappaB pathway. The invention may
CC be useful for the production of compounds with an antiinflammatory,
CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
CC vulnery activity or for gene therapy. The proteins and nucleotides are
CC useful for diagnosing, preventing, treating, or ameliorating conditions

CC or diseases associated with the NF-kappaB pathway. The condition is an
CC immune disorder, an inflammatory disorder, an inflammatory disorder
CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
CC immune activity, disorders related to aberrant acute phase responses,
CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
CC organ transplant rejection, conditions related to organ transplant
CC rejection, disorders related to aberrant signal transduction,
CC proliferating disorders, cancers and HIV propagation in cells infected
CC with other viruses. The present sequence is that of a human protein which
CC is subject to the novel association with the NF-kappaB pathway of the
CC invention. Note: This sequence does not appear in the specification but
CC was obtained by the indexer from Genbank.

XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 52
ADK82215
ID ADK82215 standard; protein; 281 AA.
XX
AC ADK82215;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human TRAIL amino acid sequence SEQ ID NO:66.
XX
KW antibody; VH domain; VL domain; TR4 binding antibody; TRAIL receptor;
KW haematological cancer; cytostatic; immunotherapy; Non-Hodgkin's lymphoma;
KW chronic myelogenous lymphoma; multiple myeloma;
KW chronic lymphocytic leukaemia; scfv; human; TRAIL;
KW TNF-related apoptosis-inducing ligand.

OS Homo sapiens.
XX
PN WO2004016753-A2.
XX
PD 26-FEB-2004.
XX
PF 15-AUG-2003; 2003WO-US025457.
XX
PR 15-AUG-2002; 2002US-0403382P.
PR 13-NOV-2002; 2002US-0425730P.

PR 06-MAY-2003; 2003US-0468050P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Salcedo T, Ruben SM, Rosen CA, Albert VA;
XX WPI; 2004-203784/19.
XX
XX Use of an antibody or its fragment the specifically binds to TR4, for the
PT preparation of a pharmaceutical composition for treating or preventing
PT hematological cancer, e.g. Non-Hodgkin's lymphoma, multiple myeloma or
PT leukemia.
XX
PS Disclosure; SEQ ID NO 66; 353pp; English.
XX
CC The present invention describes an antibody or its fragment comprising a
CC VH and VL domain that is at least 80% identical to a VH and a VL domain
CC of any of the 14 sequences given in SEQ ID NO:43 to 56, or a VH and a VL
CC domain of an antibody expressed by any one of the cell lines contained in
CC American Type Culture Collection (ATCC) Deposit numbers PTA-3571, PTA-
CC 3570 and PTA-3675, where the antibody specifically binds TR4 (TRAIL
CC receptor). Also described is a pharmaceutical composition for treating or
CC preventing haematological cancer, comprising the antibody or its fragment
CC and a member selected from ibritumomab tiuxetan, imatinib mesylate,
CC bortezomid, and a smac peptide or polypeptide. The antibody has
CC cytostatic activity, and can be used in immunotherapy. The antibody or
CC its fragment can be used for the preparation of a pharmaceutical
CC composition for treating or preventing haematological cancer, e.g. Non-
CC Hodgkin's lymphoma, chronic myelogenous lymphoma, multiple myeloma, or
CC chronic lymphocytic leukaemia. The present sequence represents human
CC tumour necrosis factor (TNF) related apoptosis-inducing ligand (TRAIL),
CC which is used in the exemplification of the present invention.

XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 53
ADS88000
ID ADS88000 standard; protein; 281 AA.
XX
AC ADS88000;

XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour treatment-related human protein sequence SeqID36.
XX
KW tumour inhibition; tumour treatment; metastasis; infectious lesion;
KW antigen presenting cell; immunostimulatory cytokine; cytostatic;
KW vulneryary; immunomodulator; melanoma; hepatoma; adenocarcinoma;

KW colorectal cancer; basal cell cancer; oral cancer; nasopharyngeal cancer;
KW laryngeal cancer; bladder cancer; head cancer; neck cancer;
KW renal cell cancer; pancreatic cancer; pulmonary cancer; cervical cancer;
KW ovarian cancer; oesophageal cancer; gastric cancer; prostate cancer;
XX testicular cancer; breast cancer; human.

OS Homo sapiens.
XX
XX WO2004034995-A2.
XX
XX 29-APR-2004.
XX
XX 15-OCT-2003; 2003WO-US032827.
PF
XX 15-OCT-2002; 2002US-0418865P.
PR
XX (UYPI-) UNIV PITTSBURGH.

PA
PI Lotze MT, Tahara H;
XX
XX WPI; 2004-365083/34.
DR N-PSDB; ADS87999.

XX Inhibiting or treating a tumor, metastasis or infectious lesion comprises
PT administering into or near site of a tumor or infectious lesion an
PT antigen presenting cell and an immunostimulatory cytokine or a nucleic
PT acid encoding the cytokine.
XX

PS Disclosure; SEQ ID NO 36; 169pp; English.

XX
CC This invention relates to a novel method of inhibiting or treating a
CC tumour, metastasis or infectious lesion in a subject which comprises
CC administering into or near a site of a tumour or infectious lesion in a
CC subject an antigen presenting cell and an immunostimulatory cytokine or a
CC nucleic acid encoding the cytokine. The invention may be useful for the
CC production of compounds with a cytostatic or vulnerary activity acting as
CC immunomodulators. The method is useful in inhibiting or treating a
CC tumour, metastasis or infectious lesion in a subject, where the size of
CC the tumour, metastasis (where number is also decreased) or infectious
CC lesion is decreased. The tumour is selected from melanoma, hepatoma,
CC adenocarcinoma, colorectal cancer, basal cell cancer, oral cancer,
CC nasopharyngeal cancer, laryngeal cancer, bladder cancer, head and neck
CC cancer, renal cell cancer, pancreatic cancer, pulmonary cancer, cervical
CC cancer, ovarian cancer, oesophageal cancer, gastric cancer, prostate
CC cancer, testicular cancer and breast cancer. The present sequence is that
CC of a protein which is related to the invention.

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAMMEVQGGPSLQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
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QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQQNISPLVREGPQ 120
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QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 |||||
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
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QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDILLMKARNSCWSKDAEYGLY 240
 |||||
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 |||||
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFILVG 281
 |||||
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFILVG 281
 |||||

RESULT 54
ABO84415
ID ABO84415 standard; protein; 281 AA.
XX
AC ABO84415;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated protein HP7-053.3.
XX
KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;
KW lymphoma; CAP.
XX
OS Homo sapiens.
XX
PN WO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-0038838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
PA (SAGR-) SAGRES DISCOVERY INC.

XX Morris DW, Morris DW, Malandro MS;
PI
XX WPI; 2004-652914/63.
DR N-PSDB; ABD32555.
XX
PT New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
PS claim 18; seqid 36; 310pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells(comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

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CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 281 AA;

Query Match      100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

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QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
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QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 240
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QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 55
ADP23388
ID ADP23388 standard; protein; 281 AA.
XX
AC ADP23388;
XX
DT 18-NOV-2004 (first entry)
XX
DE PRO polypeptide SEQ ID NO:566.
XX
KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX
OS Unidentified.
XX
PN WO2004041170-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034312.
XX
PR 01-NOV-2002; 2002US-0423394P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-419628/39.
DR N-PSDB; ADP23387.
XX
PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 7; SEQ ID NO 566; 2940pp; English.
XX
CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
```

```
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 281 AA;

Query Match      100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

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Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Job time : 166 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 11:53:43 ; Search time 54 Seconds
(without alignments)
1798.816 Million cell updates/sec

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Perfect score: 1478
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1478	100.0	281	8 US-08-916-625B-6	Sequence 6, Appli
2	1478	100.0	281	8 US-08-971-317A-8	Sequence 8, Appli
3	1478	100.0	281	9 US-09-813-329-17	Sequence 17, Appli
4	1478	100.0	281	9 US-09-193-663-8	Sequence 8, Appli
5	1478	100.0	281	9 US-09-934-465-1	Sequence 1, Appli
6	1478	100.0	281	10 US-09-919-039-118	Sequence 118, App
7	1478	100.0	281	13 US-10-011-125-4	Sequence 4, Appli
8	1478	100.0	281	13 US-10-001-054-54	Sequence 54, Appli
9	1478	100.0	281	14 US-10-093-766-54	Sequence 54, Appli
10	1478	100.0	281	14 US-10-174-654-11	Sequence 11, Appli
11	1478	100.0	281	14 US-10-151-882-41	Sequence 41, Appli
12	1478	100.0	281	14 US-10-218-547-20	Sequence 20, Appli
13	1478	100.0	281	14 US-10-322-673-72	Sequence 72, Appli

14	1478	100.0	281	14	US-10-139-785-66	Sequence 66, Appli
15	1478	100.0	281	14	US-10-310-793-26	Sequence 26, Appli
16	1478	100.0	281	15	US-10-279-687-8	Sequence 8, Appli
17	1478	100.0	281	15	US-10-292-486-5	Sequence 5, Appli
18	1478	100.0	281	15	US-10-333-712-1	Sequence 1, Appli
19	1478	100.0	281	15	US-10-662-429-2	Sequence 2, Appli
20	1478	100.0	281	15	US-10-202-062-20	Sequence 20, Appli
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25	1478	100.0	281	16	US-10-755-889-210	Sequence 210, App
26	1478	100.0	281	16	US-10-491-326-1	Sequence 1, Appli
27	1478	100.0	281	17	US-10-771-254-1	Sequence 1, Appli
28	1478	100.0	281	17	US-10-855-559-2	Sequence 2, Appli
29	1478	100.0	281	17	US-10-451-200-5	Sequence 5, Appli
30	1478	100.0	281	17	US-10-495-353-1	Sequence 1, Appli
31	1478	100.0	281	17	US-10-652-979-1	Sequence 1, Appli
32	1469	99.4	279	13	US-10-066-209-3	Sequence 3, Appli
33	1456	98.5	279	16	US-10-367-094-22	Sequence 22, Appli
34	1437	97.2	283	17	US-10-978-203-23	Sequence 23, Appli
35	1269.5	85.9	246	9	US-09-855-544A-13	Sequence 13, Appli
36	1017	68.8	208	9	US-09-855-544A-16	Sequence 16, Appli
37	988	66.8	253	15	US-10-652-244-11	Sequence 11, Appli
38	988	66.8	256	15	US-10-652-244-13	Sequence 13, Appli
39	985.5	66.7	461	15	US-10-389-223A-6	Sequence 6, Appli
40	982	66.4	480	15	US-10-389-223A-4	Sequence 4, Appli
41	978	66.2	614	15	US-10-389-223A-2	Sequence 2, Appli
42	964.5	65.3	296	14	US-10-185-425-5	Sequence 5, Appli
43	937.5	63.4	188	9	US-09-855-544A-14	Sequence 14, Appli
44	930	62.9	291	10	US-09-873-829-6	Sequence 6, Appli
45	930	62.9	291	13	US-10-017-910-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Publication No. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; TITLE OF INVENTION: RECEPTOR, TR6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50008-1
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-916-625B-6

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Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-08-971-317A-8
; Sequence 8, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,317A
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mimi C
; REGISTRATION NUMBER: 39,046
; REFERENCE/DOCKET NUMBER: 6255.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; TELEX:

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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-8

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Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 17, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Suibb Company
; TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Mole
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 281
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; ORGANISM: Drosophila melanogaster
US-09-813-329-17

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Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVREGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSDAEYGLY 240

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Db 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 4
US-09-193-663-8
; Sequence 8, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.02
; CURRENT APPLICATION NUMBER: US/09/193,663
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-8

Query Match 100.0%; Score 1478; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPG 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 5
US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match 100.0%; Score 1478; DB 9; Length 281;

Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPG 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 6
US-09-919-039-118
; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118

Query Match 100.0%; Score 1478; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPG 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7

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US-10-011-125-4
; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4

Query Match      100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGTCLVIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
      |||||||
Db      1 MAMMEVQGGPSLGTCLVIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY      61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLILRTSEETISTVQEKQONISPLVRERGPO 120
      |||||||
Db      61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLILRTSEETISTVQEKQONISPLVRERGPO 120

QY      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
      |||||||
Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180

QY      181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
      |||||||
Db      181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFSVSTNEHLIDMDHEASFFGAFLVG 281
      |||||||
Db      241 SIYQGGIFELKENDRIFSVSTNEHLIDMDHEASFFGAFLVG 281

RESULT 8
US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard,Audrey
; APPLICANT: Gurney,Austin
; APPLICANT: Hebert,Carolyn
; APPLICANT: Henzel,William
; APPLICANT: Kabakoff,Rhona
; APPLICANT: Shelton,David
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; TITLE OF INVENTION: CELL GROWTH
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/096891
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/096894
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100263
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/107783
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112420
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/115554
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116533
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/131294
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/218517
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/284291
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380913
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 09/403297
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/423741
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
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; PRIOR APPLICATION NUMBER: 09/802706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/866034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/882636
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US99/00106
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/08615
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28634
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00376
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/06884
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/13705
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/14941
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/22031
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678

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; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US01/27099
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-54

Query Match 100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGGTCLVIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MAMMEVQGGPSLGGTCLVIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWKDAEYGLY 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 9
US-10-093-766-54
; Sequence 54, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54

Query Match 100.0%; Score 1478; DB 14; Length 281;

Best Local Similarity 100.0%; Pred. No. 1.3e-128;		
Matches 281;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVTVYVYFTNELKQMDKYSKSGIACFLKE 60
Db	1	MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVTVYVYFTNELKQMDKYSKSGIACFLKE 60
Qy	61	DDSYWDPNDEESMNSPCQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
Db	61	DDSYWDPNDEESMNSPCQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
Qy	121	RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
Db	121	RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
Qy	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSPDPILLMK SARNSCWSKDAEYGLY 240
Db	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSPDPILLMK SARNSCWSKDAEYGLY 240
Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFILVG 281
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFILVG 281

; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-218-547-20

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60
|
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
|
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180
|
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 240
|
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 13
US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-72

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60
|
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
|
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180
|
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 240
|
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14
US-10-139-785-66
; Sequence 66, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-66

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60
|
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
|
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180
|
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60
|
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
|
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180
|
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 240
|
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14
US-10-139-785-66
; Sequence 66, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-66

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60
|
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
|
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180
|
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180

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Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
QY      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
Db      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 15
US-10-310-793-26
; Sequence 26, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-310-793-26

Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60
Db      1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60

QY      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

QY      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180

QY      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
Db      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240

US-10-662-431-2.rapb
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Db      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 16
US-10-279-687-8
; Sequence 8, Application US/10279687
; Publication No. US20030211509A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.C2
; CURRENT APPLICATION NUMBER: US/10/279,687
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 10/105,738
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/193,663
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/065,916
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-687-8

Query Match      100.0%; Score 1478; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60
Db      1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60

QY      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

QY      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180

QY      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
Db      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240

US-10-292-486-5
; Sequence 5, Application US/10292486
; Publication No. US20030228309A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
; FILE REFERENCE: PF532P1
; CURRENT APPLICATION NUMBER: US/10/292,486
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/403,376
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/377,973
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/331,309
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; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/986,149
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,359
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/295,018
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/252,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/248,847
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/246,612
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-486-5

Query Match      100.0%; Score 1478; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60
Db      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60

QY      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLIRTSEETISTVQEKQQNISPLVRERGPG 120
Db      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLIRTSEETISTVQEKQQNISPLVRERGPG 120

QY      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY      181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNCSWSKDAEYGLY 240
Db      181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNCSWSKDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEADSFFGAFLVG 281
Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEADSFFGAFLVG 281
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RESULT 18
US-10-333-712-1
; Sequence 1, Application US/10333712
; Publication No. US20040005314A1
; GENERAL INFORMATION:
; APPLICANT: Escandon, Enrique
; APPLICANT: Fox, Judith A.
; APPLICANT: Kelley, Sean K.
; APPLICANT: Xiang, Hong
; TITLE OF INVENTION: APO-2L RECEPTOR AGONIST AND CPT-11 SYNERGISM
; FILE REFERENCE: P1838R1
; CURRENT APPLICATION NUMBER: US/10/333,712
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: PCT/US01/23691
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,256
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-333-712-1

Query Match      100.0%; Score 1478; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60
Db      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60

QY      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLIRTSEETISTVQEKQQNISPLVRERGPG 120
Db      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLIRTSEETISTVQEKQQNISPLVRERGPG 120

QY      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY      181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNCSWSKDAEYGLY 240
Db      181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNCSWSKDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEADSFFGAFLVG 281
Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEADSFFGAFLVG 281

RESULT 19
US-10-662-429-2
; Sequence 2, Application US/10662429
; Publication No. US20040038347A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,429
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-429-2

Query Match      100.0%; Score 1478; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60
Db      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60

QY      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLIRTSEETISTVQEKQQNISPLVRERGPG 120
```

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Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
```

```
RESULT 20
US-10-202-062-20
; Sequence 20, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-202-062-20
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Query Match 100.0%; Score 1478; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGTCLVLIIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGTCLVLIIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
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RESULT 21
US-10-662-431-2
; Sequence 2, Application US/10662431
; Publication No. US20040047864A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
```

```
;
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,431
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-431-2
```

```
Query Match 100.0%; Score 1478; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGTCLVLIIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGTCLVLIIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERG 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
```

```
RESULT 22
US-10-662-430-2
; Sequence 2, Application US/10662430
; Publication No. US20040048340A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```



```
Db      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
      |||||||
Qy      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
      |||||||
Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
      |||||||

RESULT 25
US-10-755-889-210
; Sequence 210, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 210
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-210

Query Match      100.0%; Score 1478; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTTNELKQMDKYSKSGIACFLKE 60
      |||||||
Db      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTTNELKQMDKYSKSGIACFLKE 60
      |||||||

Qy      61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPO 120
      |||||||
Db      61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPO 120
      |||||||

Qy      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
      |||||||
Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
      |||||||

Qy      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
      |||||||
Db      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
      |||||||

RESULT 26
US-10-491-326-1
; Sequence 1, Application US/10491326
; Publication No. US20040186051A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: Robert F. Kelley, Stephanie H. Lindstrom
; TITLE OF INVENTION: AP0-2 Ligand Variants and Uses Thereof
; FILE REFERENCE: P18581
; CURRENT APPLICATION NUMBER: US/10/491,326
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 60/326,622
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
```

```
; ORGANISM: Homo Sapiens
US-10-491-326-1

Query Match      100.0%; Score 1478; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTTNELKQMDKYSKSGIACFLKE 60
      |||||||
Db      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTTNELKQMDKYSKSGIACFLKE 60
      |||||||

Qy      61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPO 120
      |||||||
Db      61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPO 120
      |||||||

Qy      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
      |||||||
Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
      |||||||

Qy      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
      |||||||
Db      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
      |||||||

RESULT 27
US-10-771-254-1
; Sequence 1, Application US/10771254
; Publication No. US20050020498A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: Flores, Heather
; APPLICANT: Lin, Tanya P.
; APPLICANT: Pai, Roger
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Matthews, Timothy C.
; TITLE OF INVENTION: Apo-2 Ligand/TRAIL FORMULATIONS
; FILE REFERENCE: P1857R1P1
; CURRENT APPLICATION NUMBER: US/10/771,254
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/338,249
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/US02/36251
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-254-1

Query Match      100.0%; Score 1478; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTTNELKQMDKYSKSGIACFLKE 60
      |||||||
Db      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTTNELKQMDKYSKSGIACFLKE 60
      |||||||

Qy      61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPO 120
      |||||||
Db      61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPO 120
      |||||||

Qy      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
      |||||||
Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
      |||||||

Qy      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
      |||||||
Db      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSKDAEYGLY 240
      |||||||
```

```
QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
|||||
Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 28
US-10-855-559-2
; Sequence 2, Application US/10855559
; Publication No. US20050031593A1
; GENERAL INFORMATION:
; APPLICANT: Harding, Thomas
; APPLICANT: Jooss, Karin
; APPLICANT: Lalani, Alshad
; APPLICANT: Donahue, Brian
; TITLE OF INVENTION: Method for Treating Cancer By Vector-Mediated Delivery of
; TITLE OF INVENTION: One or More Anti-Angiogenic or Proapoptotic Genes
; FILE REFERENCE: 3802-094-27
; CURRENT APPLICATION NUMBER: US/10/855,559
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/475,006
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-855-559-2

Query Match      100.0%; Score 1478; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
|||||
Db      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60

QY      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
|||||
Db      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

QY      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
|||||
Db      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
|||||
Db      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
|||||
Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 29
US-10-451-200-5
; Sequence 5, Application US/10451200
; Publication No. US20050048645A1
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; TITLE OF INVENTION: METHOD OF TREATING OR PREVENTING DISEASE CHARACTERIZED BY CRYPTO
; TITLE OF INVENTION: NEOFORMANS INFECTION
; FILE REFERENCE: 2966-WO
; CURRENT APPLICATION NUMBER: US/10/451,200
; CURRENT FILING DATE: 2003-06-21
; PRIOR APPLICATION NUMBER: US 60/259,653
; PRIOR FILING DATE: 2001-01-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-451-200-5

Query Match      100.0%; Score 1478; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
|||||
Db      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60

QY      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
|||||
Db      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

QY      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
|||||
Db      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
|||||
Db      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
|||||
Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 30
US-10-495-353-1
; Sequence 1, Application US/10495353
; Publication No. US20050080006A1
; GENERAL INFORMATION:
; APPLICANT: FLORES, Heather
; APPLICANT: LIN, Tanya P.
; APPLICANT: PAI, Roger
; APPLICANT: SHAHROKH, Zahra
; APPLICANT: MATTHEWS, Timothy
; TITLE OF INVENTION: Apo-2 LIGAND/TRAIL FORMULATIONS
; FILE REFERENCE: P1857R1
; CURRENT APPLICATION NUMBER: US/10/495,353
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: PCT/US02/36251
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/338,249
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-495-353-1

Query Match      100.0%; Score 1478; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
|||||
Db      1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60

QY      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
|||||
Db      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

QY      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
|||||
Db      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
|||||
Db      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
```

Qy	241	SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGFLVG	281
Db	241	SIYOGFIFELKENDRIFVSVTNEHLIDMDHEASFFGFLVG	281

RESULT 31

```

US-10-652-979-1
; Sequence 1, Application US/10652979
; Publication No. US20050089958A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Schwall, Ralph H.
; TITLE OF INVENTION: Apo-2 Ligand
; FILE REFERENCE: P0978P3C1
; CURRENT APPLICATION NUMBER: US/10/652,979
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 09/060,533
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: US 09/007,886
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 08/780,496
; PRIOR FILING DATE: 1997-01-08
; PRIOR APPLICATION NUMBER: US 60/009,755
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-979-1

```

```
Query Match      100.0%; Score 1478; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1	MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYKSGIACFLKE	60
Db	1		60
QY	61	DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMIILRTSEETISTVQEKQONISPLVRERGPQ	120
Db	61		120
QY	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG	180
Db	121		180
QY	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY	240
Db	181		240
QY	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281
Db	241		281

RESULT 32

US-10-066-209-3
; Sequence 3, Application US/10066209
; Publication No. US20020115110A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030-D1
; CURRENT APPLICATION NUMBER: US/10/066,209
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/072,993
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980

```

; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279

```

```
Query Match          99.4%; Score 1469; DB 13; Length 279;
Best Local Similarity 100.0%; Pred. No. 8.5e-128;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	3	MMEVQGPGSLGQTCLVIIVIFTVLQLSCLVAVTYYFTNELKQMDDKYSGIACFLKEDD	62
Dd	1	MMEVQGPGSLGQTCLVIIVIFTVLQLSCLVAVTYYFTNELKQMDDKYSGIACFLKEDD	60
QY	63	SYWDPNDEESMNSPCWKVQKLRLVRKMILRTSEETISTVQEKKQNISPLVRERGPQRV	122
Dd	61	SYWDPNDEESMNSPCWKVQKLRLVRKMILRTSEETISTVQEKKQNISPLVRERGPQRV	120
QY	123	AAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGLVVIHEKGFY	182
Dd	121	AAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGLVVIHEKGFY	180
QY	183	YIYSQTYFRFQEEIKENTKNDKOMVQYIYKYTSYPDPILLMKSAARNCSWSKDAEYGLYSI	242
Dd	181	YIYSQTYFRFQEEIKENTKNDKOMVQYIYKYTSYPDPILLMKSAARNCSWSKDAEYGLYSI	240
QY	243	YQGGIFELKENDRIFVSVTNEHLIDMDHEADSFFGAFLVG	281
Dd	241	YQGGIFELKENDRIFVSVTNEHLIDMDHEADSFFGAFLVG	279

RESULT 33

```

US-10-367-094-22
; Sequence 22, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-094-22

```

Query Match 98.5%; Score 1456; DB 16; Length 279;
Best Local Similarity 99.3%; Pred. No. 1.4e-126;
Matches 279; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy	1	MAMMEVQGPGSLGQTCLIVIFTVLQLSCLVAVTYVFTNELKMQMDKYSKSGIACFLKE	60
D _b	1	MAMMEVQGPGSLGQTCLIVIFTVLQLSCLVAVTYVFTNELKMQMDKYSKSGIACFLKE	60
Qy	61	DDSYWDPNDEESMNSPCWQVKWLRLVRKMILRTSEETISTVQEKKQNISPLVRERGPQ	120
D _b	61	DDSYWDPNDEESMNSPCWQVKWLRLVRKMILRTSEETISTVQEKKQNISPLVRERGPQ	120
Qy	121	RVAAHITGTGRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG	180
D _b	121	RVAAHITGTGRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG	180
Qy	181	FYYIYSQTYFRFQEEIKENTKNDKQMVGIIYKYTSPDPIILLMKARSNCWSKDAEYGly	240

Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYG-- 238

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||

Db 239 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279

RESULT 34

US-10-978-203-23

; Sequence 23, Application US/10978203

; Publication No. US20050112666A1

; GENERAL INFORMATION:

; APPLICANT: Chicheportiche, Yves

; APPLICANT: Browning, Jeffrey

; TITLE OF INVENTION: Tumor Necrosis Factor Related Ligand

; FILE REFERENCE: A003

; CURRENT APPLICATION NUMBER: US/10/978,203

; CURRENT FILING DATE: 2004-10-29

; PRIOR APPLICATION NUMBER: 60/023,541

; PRIOR FILING DATE: 1996-08-07

; PRIOR APPLICATION NUMBER: 60/028,515

; PRIOR FILING DATE: 1996-10-18

; PRIOR APPLICATION NUMBER: 60/040,820

; PRIOR FILING DATE: 1997-03-18

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 23

; LENGTH: 283

; TYPE: PRT

; ORGANISM: homo sapien

US-10-978-203-23

Query Match 97.2%; Score 1437; DB 17; Length 283;

Best Local Similarity 97.5%; Pred. No. 8.1e-125;

Matches 278; Conservative 0; Mismatches 1; Indels 6; Gaps 2;

Qy 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQM QDKYSKSGIACFLKE 60
|||||

Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQM QDKYSKSGIACFLKE 60
|||||

Qy 61 DDSYWDPNDEESMNSPC-----WQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRE 116
|||||

Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRE 120
|||||

Qy 117 RGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVI 176
|||||

Db 121 RGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVI 180
|||||

Qy 177 HEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAE 236
|||||

Db 181 HEKGFYIYSQTYFRFQEEIKENTKNDKQMVVYIYKYTSYDPDPILLMKSARNSCWSKDAE 240
|||||

Qy 237 YGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||

Db 241 YG--SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 283
|||

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	305.5	23.7		214	2	Q9DDZ5	Q9ddz5 brachydanio
2	291	22.6		63	2	Q6JSD9	Q6jds9 homo sapien
3	175.5	13.6		169	2	Q9WV90	Q9wv90 marmota mon
4	163.5	12.7		131	2	Q6J3Q6	Q6j3q6 canis famil
5	160	12.4		174	1	TN15_HUMAN	Q95150 homo sapien
6	159.5	12.4		240	1	TN14_HUMAN	Q43557 homo sapien
7	157	12.2		154	2	Q8MJ19	Q8mj19 macaca mula
8	152.5	11.8		239	1	TN14_MOUSE	Q9qyh9 mus musculu
9	151.5	11.8		227	2	Q7T2Q3	Q7t2q3 cyprinus ca
10	144.5	11.2		216	2	O70332	O70332 mesocricetu
11	143	11.1		241	2	Q6U817	Q6u817 lateolabrax
12	141	11.0		231	2	Q8AW02	Q8aw02 cyprinus ca
13	137.5	10.7		232	2	Q80XA4	Q80xa4 peromyscus
14	137.5	10.7		234	2	Q6T9C7	Q6t9c7 brachydanio
15	136.5	10.6		235	1	TNFA_RABIT	P04924 oryctolagus
16	135	10.5		156	2	Q91ZL4	Q91zl4 sigmodon hi
17	135	10.5		215	2	Q9BEE8	Q9bee8 erinaceus e
18	135	10.5		217	2	Q9ERG6	Q9erg6 peromyscus
19	134.5	10.5		204	1	TNFB_PIG	P26445 sus scrofa
20	132.5	10.3		234	1	TNFA_CAVPO	P51435 cavia porce
21	130.5	10.1		222	2	Q7T1U4	Q7t1u4 pagrus majo
22	130	10.1		232	1	TNFA_PIG	P23563 sus scrofa
23	129.5	10.1		235	1	TNFA_PERLE	P36939 peromyscus
24	128	9.9		230	2	Q8JG37	Q8jg37 ictalurus p
25	127.5	9.9		204	1	TNFB_BOVIN	Q06600 bos taurus
26	126.5	9.8		225	2	Q9IB42	Q9ib42 paralichthy
27	126	9.8		234	1	TNFA_HORSE	P29553 equus cabal
28	125	9.7		215	2	Q99ND1	Q99nd1 sciurus vul
29	125	9.7		233	1	TNFA_MARMO	Q35734 marmota mon
30	124	9.6		216	2	Q9BEC4	Q9bec4 talpa europ
31	123.5	9.6		216	2	Q9BEC9	Q9bec9 ochotona pr


```

RN RP SEQUENCE FROM N.A.
RX MEDLINE=22937400; PubMed=14576776;
RA Arnault D., Petit F., Lelievre J.D., Lecossier D., Hance A.,
RA Monceaux V., Ho Tsong Fang R., Huntrel B., Ameisen J.C., Estaquier J.;
RT "Caspase-dependent and -independent T-cell death pathways in
RT pathogenic simian immunodeficiency virus infection: relationship to
RT disease progression.";
RL Cell Death Differ. 10:1240-1252(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Hance A.J., Lecossier D., Estaquier J.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF530076; AAM95636.1; -.
DR HSSP; P50591; 1D2Q.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas_ligand.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 17410 MW; 971A43779E029449 CRC64;

Query Match      12.2%; Score 157; DB 2; Length 154;
Best Local Similarity 27.4%; Pred. No. 4.5e-05;
Matches 46; Conservative 33; Mismatches 65; Indels 24; Gaps 6;

QY 57 TSEETISTVQEKQNISPLVRERGQPORVAAHITGTRGSNTLSSPNKNEKALGRKINSW 116
Db TSQKHTASSLEKIQGHSPPEKEQRKVAHLTG-----KPNSRSMPL-----EW 52

QY 117 ESSRSRGHSFLSNLHNLNGELVIHEKGFIYIYSQT YFRFOBEIKENTKNDKQMVOYIY-KY 175
Db EDT-YGIVLLSGVKYKKGLVINETGLYFVYSKVYFRGQ-----SCTNPLSHKVVMRN 105

QY 176 TSYPDPILLMKSRNSCSWSDAEYGLYSIQGGIFELKENDRIFVSVT 223
Db SKYPQDLVMMEGKMMS-YCTTGQMWAAHSSYLGAVENTLSADHLVNVVS 152

RESULT 8
TN14 MOUSE
ID TN14_MOUSE STANDARD; PRT; 239 AA.
AC Q9QYH9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 14.
GN Name=Tnfsf14; Synonyms=LIGHT;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20165223; PubMed=10700230; DOI=10.1038/73136;
RA Tamada K., Shimozaki K., Chapoval A.I., Zhu G., Sica G., Flies D.,
RA Boone T., Hsu H., Fu Y.-X., Nagata S., Ni J., Chen L.;
RT "Modulation of T-cell-mediated immunity in tumor and graft-versus-host
RT disease models through the LIGHT co-stimulatory pathway.";
RL Nat. Med. 6:283-289(2000).
```

RN	[2]	SEQUENCE FROM N.A.	
RP		TISSUE=Fetal liver;	
RC		MEDLINE=20354998; PubMed=10894944;	
RX		Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;	
RA		"Molecular cloning and characterization of a mouse homolog of human	
RT		TNFSF14, a member of the TNF superfamily.";	
RT		Cytogenet. Cell Genet. 89:89-91(2000).	
RL		[3]	
RN		SEQUENCE FROM N.A.	
RP		TISSUE=Lymphoma;	
RC		Force W.R., Todd P.K., Mikayama T.;	
RA		"Mouse LIGHT; molecular genetics, ligand binding and expression.";	
RT		Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.	
RL		-!- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the	
CC		decoy receptor TNFRSF6B modulates its effects. Activates NFKB and	
CC		stimulates the proliferation of T cells.	
CC		-!- SUBUNIT: Homotrimer (By similarity).	
CC		-!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By	
CC		similarity).	
CC		-!- PTM: The soluble form derives from the membrane form by	
CC		proteolytic processing.	
CC		-!- SIMILARITY: Belongs to the tumor necrosis factor family.	
CC		-----	
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC		between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC		the European Bioinformatics Institute. There are no restrictions on its	
CC		use by non-profit institutions as long as its content is in no way	
CC		modified and this statement is not removed. Usage by and for commercial	
CC		entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC		or send an email to license@isb-sib.ch).	
CC		-----	
DR		EMBL; AF123385; AAF76453.1; -.	
DR		EMBL; AB029155; BAA88559.1; -.	
DR		EMBL; AF227533; AAF36722.1; -.	
DR		HSSP; P01375; 4TSV.	
DR		MGD; MGI:1355317; Tnfsf14.	
DR		GO; GO:0043027; F:caspase inhibitor activity; ISS.	
DR		GO; GO:0005102; F:receptor binding; ISS.	
DR		GO; GO:0001719; P:inhibition of caspase activation; ISS.	
DR		GO; GO:0008588; P:release of cytoplasmic sequestered NF-kappaB; ISS.	
DR		GO; GO:0007165; P:signal transduction; ISS.	
DR		GO; GO:0043029; P:T-cell homeostasis; ISS.	
DR		GO; GO:0042098; P:T-cell proliferation; ISS.	
DR		InterPro; IPR006053; TNF_abc.	
DR		InterPro; IPR006052; TNF_family.	
DR		InterPro; IPR008983; TNF_like.	
DR		InterPro; IPR003636; TNF_subf.	
DR		Pfam; PF00229; TNF; 1.	
DR		PRINTS; PR01234; TNECROSISFCT.	
DR		ProDom; PD002012; TNF_subf; 1.	
DR		PROSITE; PS00251; TNF_1; FALSE_NEG.	
DR		PROSITE; PS50049; TNF_2; 1.	
KW		Cytokine; Glycoprotein; Signal-anchor; Transmembrane.	
FT		CHAIN 1 239 Tumor necrosis factor ligand superfamily	
FT		member 14, membrane form.	
FT		CHAIN ?82 239 Tumor necrosis factor ligand superfamily	
FT		member 14, soluble form.	
FT		DOMAIN 1 37 Cytoplasmic (Potential).	
FT		TRANSMEM 38 58 Signal-anchor for type II membrane	
FT		protein (Potential).	
FT		DOMAIN 59 239 Extracellular (Potential).	
FT		SITE 81 82 Cleavage (Potential).	
FT		DISULFID 152 187 Potential.	
FT		CARBOHYD 100 100 N-linked (GlcNAc. . .) (Potential).	
FT		CARBOHYD 191 191 N-linked (GlcNAc. . .) (Potential).	
SEQ		SEQUENCE 239 AA; 26338 MW; 217874AC71AD6BE3 CRC64;	
Query Match		11.8%; Score 152.5; DB 1; Length 239;	
Best Local Similarity		29.2%; Pred. No. 0.00019;	
Matches		47; Conservative 25; Mismatches 72; Indels 17; Gaps 6;	
OY	85	AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKGFY 144	

Db	93	AAHLTGANASLIGIGP-----LLWE-TRLGLAFLRGLTYHDGALVTMEPGYY	139
QY	145	YIYSQTYFRFQEEIKENTKNDKQMVOYIYKYTS-YPDPILLMKSAARNSCWSKDAEYGLY-	202
Db	140	YVYSKVQLS-GVGCPOGLANGLPITHGLYKRTSRYPKKELELLVSRSPCCGRANSSRVWWD	198
QY	203	SIYQGGIFELKENDRIFVSVTNEHLI-DMDHEASFFGAFV	242
Db	199	SSFGLGGVVHLEAGEEVVRVPGNRLVPRDGTGRSYFGAFMV	239
RESULT 9			
Q7T2Q3			
ID	Q7T2Q3	PRELIMINARY;	PRT; 227 AA.
AC	Q7T2Q3;		
DT	01-OCT-2003	(TrEMBLrel. 25, Created)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	Tumor necrosis factor-3 alpha.		
GN	Name=TNF-3alpha;		
OS	Cyprinus carpio (Common carp).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Cyprinus.		
OX	NCBI_TaxID=7962;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Head kidney;		
RX	PubMed=15145420; DOI=10.1016/j.fsi.2003.11.001;		
RA	Savan R., Sakai M.;		
RT	"Presence of multiple isoforms of TNF alpha in carp (Cyprinus carpio		
RT	L.): genomic and expression analysis.";		
RL	Fish Shellfish Immunol. 17:87-94(2004).		
DR	EMBL; AB112424; BAC77690.1; --		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.		
DR	GO; GO:0006955; P:immune response; IEA.		
DR	InterPro; IPR006052; TNF family.		
DR	InterPro; IPR008983; TNF_like.		
DR	InterPro; IPR003636; TNF_subf.		
DR	Pfam; PF00229; TNF; 1.		
DR	ProDom; PD002012; TNF subf; 1.		
DR	SMART; SM00207; TNF; 1.		
DR	PROSITE; PS50049; TNF 2; 1.		
SQ	SEQUENCE 227 AA; 25226 MW; 010BC2B1E8D7265E CRC64;		
Query Match 11.8%; Score 151.5; DB 2; Length 227;			
Best Local Similarity 25.3%; Pred. No. 0.00021;			
Matches 45; Conservative 34; Mismatches 68; Indels 31; Gaps 7			
QY	75	LVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG	134
Db	67	LSKENVTSKVAIHLSGA-----YEPDVSKNNIDWKQNDQDGAFVSGGLKLVD	113
QY	135	ELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVOYIYKYTSYPD-----PILLM	188
Db	114	EIIIPNDGIYFIYSQVSFHI--SCKNDMTEDQEVHMVSHAVFHYSDFFGIYKP--LIRAA	169
QY	189	RNSCW----SKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF	240
Db	170	RSACVHASNTEDVWYD--TIYLGAAFSLRAGDKLCTKTTTELLPRVETDNAKTFFGVF	225
RESULT 10			
O70332			
ID	O70332	PRELIMINARY;	PRT; 216 AA.
AC	O70332;		
DT	01-AUG-1998	(TrEMBLrel. 07, Created)	
DT	01-AUG-1998	(TrEMBLrel. 07, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Tumor necrosis factor-alpha (Fragment).		
OS	Mesocricetus auratus (Golden hamster).		

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC	Mesocricetus.
OX	NCBI_TaxID=10036;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Spleen;
RX	MEDLINE=98234044; PubMed=9573100;
RA	Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT	"Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT	analysis of cytokine mRNA expression in experimental visceral
RT	leishmaniasis.";
RL	Infect. Immun. 66:2135-2142(1998).
DR	EMBL; AF046215; AAC40100.1; -.
DR	HSSP; P06804; 2TNF.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR	GO; GO:0006955; P:immune response; IEA.
DR	InterPro; IPR006053; TNF_abc.
DR	InterPro; IPR002959; TNF_alpha.
DR	InterPro; IPR006052; TNF_family.
DR	InterPro; IPR008983; TNF_like.
DR	InterPro; IPR003636; TNF_subf.
DR	Pfam; PF00229; TNF; 1.
DR	PRINTS; PR01234; TNECROSISFCT.
DR	PRINTS; PR01235; TNFALPHA.
DR	ProDom; PD002012; TNF_subf; 1.
DR	SMART; SM00207; TNF; 1.
DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; PS50049; TNF_2; 1.
FT	NON_TER 1
FT	NON_TER 216
SQ	SEQUENCE 216 AA; 23793 MW; BADAE3F83F45B533 CRC64;
Query Match 11.2%; Score 144.5; DB 2; Length 216;	
Best Local Similarity 26.9%; Pred. No. 0.00074;	
Matches 47; Conservative 28; Mismatches 63; Indels 37; Gaps 7;	
Qy	80 GPQRVAAH---ITGTRGRSNTL-SSPNSKNEKALGRKINS-----WESSRSGHSFLS 127
Db	49 GPQREEKFPNPPIIGSMGQTILTRSSSSQNSNDKVPVGHVAVNHQVVEQLEWLSHRANALLAN 108
Qy	128 NLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVOYIYK-----YTSYPD 180
Db	109 GMSLKDNLQVLPADGLYLVYSQVLFRGQ-----GCPSYVLLTHTVSRIAVSYED 157
Qy	181 PILLMKSAARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLID 229
Db	158 NVNLLSAIKSPC-PKETPEGEELKPWYEPYILGVGVFQLEKGDRLSAEVLNPKYLD 211
RESULT 11	
Q6U817	
ID	Q6U817 PRELIMINARY; PRT; 241 AA.
AC	Q6U817;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Tumor necrosis factor alpha.
OS	Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC	Moronidae; Lateolabrax.
OX	NCBI_TaxID=8164;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Qiu L., Song L., Wu L., Cai Z., Xu W., Wang L.;
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY376595; AAR02413.2; -.
DR	HSSP; P01375; 1A8M.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

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DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 231 AA; 25927 MW; 2AD8871D0B1A82F1 CRC64;

Query Match      11.0%; Score 141; DB 2; Length 231;
Best Local Similarity 23.3%; Pred. No. 0.0016;
Matches 51; Conservative 38; Mismatches 90; Indels 40; Gaps 9

QY 44 WQLRQLVRKMILRTSEETISTVQEKQQN-----ISPLVRERGPRVAAHITGTR 92
|:: :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 29 WRVCGVLLAVALCAAAAVCF TLNKSNQN QEGGNALRLTLRDHL SKENVTSKVAIHLTGA- 87
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 93 GRNSTLSSPNSKNEKALGRKINSWESSRSRGHSFLSNLHRLNGELVIHEKGFFYYIYSQTYF 152
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 88 -----YDPDVCKDNL-----DWKQNQDAFYSGGLELVDR EIIIPNDGIYFVYSQVSF 135
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 153 RFQEIEIKENTKNDKQM V-----QYIYKYTSYEDPDILLMK SARNSC-WSKDAEYGLY-S 203
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 136 HI--SCKDMTEDQDVVM SHAVLR YSESYGYKP---LFSAIRSACVHASDEDLWYNT 190
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 204 IYQGIGIFELKENDRIFSVVTNEHL--IDMDHEASPF GA F 240
|| || || || : || : || || || : || : || : || : || : || : || : ||
Db 191 IYLGA AFNLRA DR LRTETT KELL PRVESEN GKTFPGVF 229
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
Q80XA4
ID Q80XA4 PRELIMINARY; PRT; 232 AA.
AC Q80XA4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor precursor (Fragment).
GN Name=Tnf;
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RA Green R.M., Herbst M.M., Schountz T.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY249143; AAP03078.1; -.
DR HSSP; P06804; 2TNF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR002959; TNF_alpha.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Signal.
FT SIGNAL 1 Potential.
FT CHAIN 80 >232 tumor necrosis factor.
FT NON TER 232
SQ SEQUENCE 232 AA; 25704 MW; E48A9379DB4F216D CRC64;

Query Match      10.7%; Score 137.5; DB 2; Length 232;
Best Local Similarity 24.5%; Pred. No. 0.003;
Matches 45; Conservative 36; Mismatches 78; Indels 25; Gaps 8;

QY 72 ISPLVRERGPQVAAHITGTRGRSNTL-SSPN SKNEKALGRKINS-----WESSRSG 122
| | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 56 IG PQREEKEFPNNLP--IIGSMAQTLLRSSSQSSDKPV AHVVANHQVDQLEWLSSRRAN 113

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DR	Pfam; PF00229; TNF; 1.	
DR	PRINTS; PR01234; TNECROSISFCT.	
DR	ProDom; PD002012; TNF subf; 1.	
DR	SMART; SM00207; TNF; 1.	
DR	PROSITE; PS00251; TNF_1; 1.	
DR	PROSITE; PS50049; TNF_2; 1.	
KW	Cytokine; Phosphorylation; Signal-anchor; Transmembrane.	
FT	CHAIN 1 235	Tumor necrosis factor, membrane form.
FT	CHAIN 80 235	Tumor necrosis factor, soluble form.
FT	DOMAIN 1 35	Cytoplasmic (Potential).
FT	TRANSMEM 36 56	Signal-anchor for type II membrane protein (Potential).
FT	DOMAIN 57 235	Extracellular (Potential).
FT	SITE 79 80	Cleavage (by ADAM17) (By similarity).
FT	MOD_RES 2 2	Phosphoserine (by CK1) (By similarity).
FT	DISULFID 148 179	By similarity.
FT	CONFLICT 63 63	Missing (in Ref. 3).
SQ	SEQUENCE 235 AA; 25816 MW; 610177D0BD2EF871 CRC64;	
Query Match 10.6%; Score 136.5; DB 1; Length 235;		
Best Local Similarity 23.0%; Pred. No. 0.0037;		
Matches 42; Conservative 37; Mismatches 81; Indels 23; Gaps 7;		
QY	72 ISPLVREGRGQORVAAHITGTRGRSNTL-SSPNSKNEKALGRKINS-----WESSRSG 122	
Db	56 IGPQEEEQSPNNL--HLVNPVAQMVTLSASRALSDKPLAHVVANPQVEGQLQWLSQRAN 113	
QY	123 HSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYDP 181	
Db	114 ALLANGMKLTDNQLVVPADGLYLIYSQVLFSGQ-----GCRSYVLLTHTVSRFAVSYPNK 168	
QY	182 ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235	
Db	169 VNLLSAIKSPCHRETPEEAEPMAWYEPIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQV 228	
QY	236 FFG 238	
Db	229 YFG 231	

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OM protein - protein search, using sw model

Run on: June 3, 2005, 06:25:45 ; Search time 161 Seconds
(without alignments)
583.744 Million cell updates/sec

Title: US-10-662-431-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNELKQMCKYKSGIACFL.....NEHLIDMDHEASFFGAFVLG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1523986

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	958	74.4	187	8	ADN35127 Human TRA
2	953.5	74.1	220	3	AAY88630 Cell fact
3	907	70.5	173	5	ABG72258 Partial h
4	887	68.9	168	4	ABB76826 Human TRA
5	887	68.9	168	5	AAU99896 Human TNF
6	882	68.5	168	5	ABG72259 Partial h
7	878	68.2	166	3	AAB08274 Amino aci
8	866	67.3	167	6	ABR84402 TRAIL ami
9	850	66.0	161	4	AAY71985 C-termina
10	850	66.0	161	6	ABR39855 TNF famil
11	850	66.0	161	7	ADC03335 Tumour ne
12	827	64.3	212	5	AAU99301 Human TRA
13	764.5	59.4	154	7	ADI33053 Human TRA
14	764	59.4	171	8	ADO24774 Cat solub
15	764	59.4	201	8	ADO24776 Cat solub
16	746.5	58.0	188	5	AAU79599 Human TRA
17	727	56.5	139	2	AAY01518 Polypepti
18	711.5	55.3	172	8	ADO24770 Dog solub
19	711.5	55.3	207	8	ADO24772 Dog solub
20	633	49.2	172	3	AAB08275 Amino aci
21	544	42.3	169	8	ADL98264 Human TNF
22	425	33.0	121	3	AAG03752 Human sec
23	370	28.7	113	5	AAU79600 Human TRA
24	292	22.7	120	8	ADL98267 Human TNF
25	291	22.6	98	5	AAU79595 Human TRA

26	291	22.6	98	8	ABO84414	Abo84414 Human can
27	291	22.6	101	2	AAW19790	Aaw19790 Human apo
28	291	22.6	101	2	AAW56761	Aaw56761 Human TRA
29	291	22.6	101	4	AAE11032	Aae11032 Human TRA
30	291	22.6	101	6	ABU08559	Abu08559 Human TNF
31	291	22.6	101	8	ADK15500	Adk15500 Human TNF
32	291	22.6	122	8	ADL98266	Adl98266 Human TRA
33	278	21.6	56	5	AAE23263	Aae23263 Protein #
34	277	21.5	88	5	AAU79594	Aau79594 Human TRA
35	236	18.3	178	6	ADA50080	Ada50080 Human wil
36	233.5	18.1	199	5	ABG94285	Abg94285 Mouse ran
37	233.5	18.1	199	5	ABG80597	Abg80597 Mouse rec
38	233.5	18.1	199	7	ADJ82119	Adj82119 Protein f
39	232.5	18.1	152	4	AAB67248	Aab67248 Human ran
40	232.5	18.1	158	7	ADJ82134	Adj82134 Protein f
41	232.5	18.1	159	7	ADJ82117	Adj82117 Protein f
42	232.5	18.1	160	3	AAB08273	Aab08273 Amino aci
43	232.5	18.1	165	7	ADJ82136	Adj82136 Protein f
44	232.5	18.1	178	7	ADJ82116	Adj82116 Protein f
45	232.5	18.1	180	7	ADJ82133	Adj82133 Protein f

ALIGNMENTS

RESULT 1
ADN35127
ID ADN35127 standard; protein; 187 AA.
XX
AC ADN35127;
XX
DT 17-JUN-2004 (first entry)
XX
DÈ Human TRAI-1 extracellular region.
XX
KW human TRAI-1 extracellular region; antineoplastic.
XX
OS Homo sapiens.
XX
PN CN1436792-A.
XX
PD 20-AUG-2003.
XX
PF 08-FEB-2002; 2002CN-00104519.
XX
PR 08-FEB-2002; 2002CN-00104519.
XX
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX
PI Zheng D, Liu Y, Shi J;
XX
WPI; 2004-023846/03.
XX
PT New tumor necrosis factor relative cell death inducing ligand
PT extracellular region mutation polypeptide, used for an antineoplastic
PT application.
XX
PS Claim 1; SEQ ID NO 1; 15pp; Chinese.
XX
CC The present invention provides one kind of mutant 95-281 recombinant
CC soluble polypeptide (rsTRAILthr95gly-281) in human TRAIL extracellular
CC region. The preparation process and antineoplastic application of the
CC recombinant soluble polypeptide are also provided. The present sequence
CC represents human TRAI-1 extracellular region.
XX
SQ Sequence 187 AA;

Query Match 74.4%; Score 958; DB 8; Length 187;
Best Local Similarity 98.9%; Pred. No. 3e-85;
Matches 184; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 58 SEETISTVQEKQKNISPLVRGPPQVAHITGTRGRSNTLSSPNKNEKALGRKINSWE 117
|||||

Db 2 SEETISTVQEQKQONISPLVRERGPQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 61

QY 118 SSRSGHSFLSNLHRLNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS 177
|||||

Db 62 SSRSGHSFLSNLHRLNEGLVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS 121

QY 178 YPDPILLMKSAWSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 237
|||||

Db 122 YPDPILLMKSAWSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 181

QY 238 GAFLVG 243
|||||

Db 182 GAFLVG 187

RESULT 2
AAV88630
ID AAV88630 standard; protein; 220 AA.
XX
AC AAV88630;
XX
DT 22-AUG-2000 (first entry)
XX
DE Cell factor derivative TRAILD amino acid sequence.
XX
KW Cell factor derivative; TRAILD; anticancer; cancer; liver; breast;
KW kidney; leukaemia.
XX
OS Unidentified.
XX
PN CN1243748-A.
XX
PD 09-FEB-2000.
XX
PF 28-JUL-1999; 99CN-00111039.
XX
PR 28-JUL-1999; 99CN-00111039.
XX
PA (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.
XX
PI Zheng D, Liu Y, Ma Z;
XX
DR WPI; 2000-351201/31.
XX
PT New cell factor derivative causing cells to die, for anticancer therapy.
XX
PS Disclosure; Page 2; 10pp; Chinese.
XX
CC The present invention relates to a cell factor derivative (TRAILD) used
CC as an anticancer derivative. The TRAIL protein can be expressed in
CC soluble form in bacterial cytoplasm. The present sequence represents a
CC TRAILD amino acid sequence. Recombinant TRAILD fusion proteins can be
CC used in anti-cancer medicaments to treat cancer of the liver, breast, or
CC kidney. It can also be used to treat leukaemia
XX
SQ Sequence 220 AA;

Query Match 74.1%; Score 953.5; DB 3; Length 220;
Best Local Similarity 97.9%; Pred. No. 1.1e-84;
Matches 185; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 56 RTSEETISTVQEQKQONISPLVRERGPQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINS 115
:|||||

Db 32 KTSEETISTVQEQKQONISPLVRERGPQORVAAHITGTRGRSQTLSSPNSKNEKALGRKINS 91

QY 116 WESSRSGHSFLSNLHRLNGELVIH-EKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK 174
|||||

Db 92 WESSRSGHSFLSNLHRLNGELVIHKEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK 151

QY 175 YTSYPDPILLMKSAWSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEA 234
|||||

Db 152 YTSYPDPILLMKSAWSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEA 211

QY 235 SFFGAFLVG 243
|||||

Db 212 SFFGAFLVG 220

RESULT 3
ABG72258
ID ABG72258 standard; protein; 173 AA.
XX
AC ABG72258;
XX
DT 04-MAR-2003 (first entry)
XX
DE Partial human Trail protein, Trail109.
XX
KW Human; tumour related apoptosis inducing ligand; Trail109;
KW Trail prokaryotic expression system; tumour cell death.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 109
FT /note= "Encoded by CTT"
XX
PN CN1354183-A.
XX
PD 19-JUN-2002.
XX
PF 30-NOV-2001; 2001CN-00132371.
XX
PR 30-NOV-2001; 2001CN-00132371.
XX
PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
XX
PI Hu Y, Yao Y;
XX
DR WPI; 2002-751439/82.
DR N-PSDB; ABX14392.
XX
PT Tumor death induction ligand gene, gene expression protein and its
PT preparation method.
XX
PS Claim 7; Page 10 (disclosure); 17pp; Chinese.
XX
CC The present invention relates to the isolation of cDNA encoding human
CC tumour related apoptosis inducing ligand (Trail), and the Trail protein.
CC The Trail full length cDNA is cloned, and is utilised to create a Trail
CC prokaryotic expression system. The full length Trail cDNA is used to
CC respectively clone cDNA of soluble ectocytic segment Trail109 and Trail
CC 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic
CC expression systems. The prokaryotic expression systems created greatly
CC increase the expression and quantity of the Trail, Trail109, and Trail114
CC proteins, and may be useful in a new preparation for killing tumour
CC cells. The present sequence represents the partial human Trail protein,
CC Trail109
XX
SQ Sequence 173 AA;

Query Match 70.5%; Score 907; DB 5; Length 173;
Best Local Similarity 99.4%; Pred. No. 2.7e-80;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 71 NISPLVRERGPQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLH 130
|||||

Db 1 NISPLVRERGPQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLH 60

QY 131 LRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSA RN 190
|||||

Db 61 LRNGELVIHEKGFYYIYSQTYFRFQEEIKENAKNDKQMVQYIYKYTSYPDPILLMKSA RN 120

QY 191 SCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
|||||

Db 121 SCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 173

RESULT 4
ABB76826
ID ABB76826 standard; protein; 168 AA.
XX
AC ABB76826;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human TRAIL.
XX
KW Human; TRAIL; tumour necrosis factor; TNF;
KW tumour necrosis factor related apoptosis inducing ligand; TRAIL; cancer;
KW viral infection; cytostatic.
XX
OS Homo sapiens.
XX
PN KR2001019100-A.
XX
PD 15-MAR-2001.
XX
PF 25-AUG-1999; 99KR-00035354.
XX
PR 25-AUG-1999; 99KR-00035354.
XX
PA (DONG-) DONG WHA PHARM IND CO LTD.
XX
PI Cha SS, Kim JU, Lee GJ, Lim GM, Oh BH, Yoon JI, Yoon SJ;
XX
DR WPI; 2001-533833/59.
DR N-PSDB; ABL53366.
XX
PT Producing and crystallizing tumor necrosis factor related apoptosis
PT inducing ligand protein, and its three-dimensional structure.
XX
PS Claim 1; Page 14; 20pp; Korean.
XX
CC The present invention relates to a method for producing Tumour Necrosis
CC Factor (TNF) Related Apoptosis Inducing Ligand (TRAIL) protein, and for
CC crystallising the TRAIL protein and its three-dimensional structure,
CC where the TRAIL protein has improved activity, which specifically kills
CC cancer cells and cells infected by virus. The present sequence is human
CC TRAIL, which was used in the invention
XX
SQ Sequence 168 AA;

Query Match 68.9%; Score 887; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 VRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 135
Db 1 VRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 60

QY 136 LVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSK 195
Db 61 LVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSK 120

QY 196 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168

RESULT 5
AAU99896
ID AAU99896 standard; protein; 168 AA.
XX
AC AAU99896;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human TNF related apoptosis inducing ligand (TRAIL) protein.

XX TRAIL; TNF receptor apoptosis including ligand; human; SDR5;
KW tumour necrosis factor; crystal structure; TRAIL-SDR5 complex; apoptosis.
XX
OS Homo sapiens.
XX
PN WO200253727-A1.
XX
PD 11-JUL-2002.
XX
PF 10-JAN-2001; 2001WO-KR0000034.
XX
PR 29-DEC-2000; 2000KR-00085947.
XX
PA (DONG-) DONG WHA PHARM IND CO LTD.
PA (UYPO-) UNIV POHANG SCI & TECHNOLOGY.
XX
PI Chung YH, Ryu JM, Hwang YH, Yoon JI, Lim KM, Oh B, Cha S;
XX
DR WPI; 2002-583613/62.
XX
PT Novel expression vector containing an sDR5 encoding gene transformed into
PT Escherichia coli to produce SDR5 protein for crystallizing a tumor
PT necrosis factor-related apoptosis-inducing ligand-sDR5 complex.
XX
PS Claim 5; Page 70; 74pp; English.
XX
CC This invention relates to an expression vector containing the tumour
CC necrosis factor related apoptosis inducing ligand (TRAIL) protein
CC receptor SDR5. The invention also comprises a method for producing the
CC SDR5 protein from an E. coli transformed with the vector. The method of
CC the invention is useful for crystallising the TRAIL-SDR5 complex. A TRAIL
CC -SDR5 crystal complex is useful for developing recombinant proteins i.e.
CC proteins with improved stability or cytotoxic activity of a TRAIL protein
CC which involves changing the amino acid of the AA loop to increase the
CC various interactions between amino acids or from the binding site of
CC metal ions or the disulfide bonding, or changing the corresponding amino
CC acids of the homotrimer interface or homodimer interface to increase the
CC various interactions between amino acids or from the binding site of
CC metal ion or disulfide bond, or to fill the cavity. A 3 dimensional
CC structure of the TRAIL-SDR5 complex is useful for the molecular strategy
CC conferring specificity for the recognition between TNF family members and
CC TNF receptor family members and for the development of TRAIL protein,
CC which has a better stable, cytotoxic activity or an improved receptor
CC binding affinity. The present sequence represents the human tumour
CC necrosis factor receptor apoptosis including ligand (TRAIL) protein
CC sequence used in the invention
XX
SQ Sequence 168 AA;

Query Match 68.9%; Score 887; DB 5; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 VRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 135
Db 1 VRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 60

QY 136 LVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSK 195
Db 61 LVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSARNSCWSK 120

QY 196 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168

RESULT 6
ABG72259
ID ABG72259 standard; protein; 168 AA.
XX
AC ABG72259;
XX

DT 04-MAR-2003 (first entry)
XX Partial human Trail protein, Trail114.
DE
XX Human; tumour related apoptosis inducing ligand; Trail114;
KW Trail prokaryotic expression system; tumour cell death.
KW Homo sapiens.
OS
XX Key Location/Qualifiers
FH Misc-difference 104
FT /note= "Encoded by CTT"
FT
XX CN1354183-A.
PN
XX 19-JUN-2002.
PD
XX 30-NOV-2001; 2001CN-00132371.
PF
XX 30-NOV-2001; 2001CN-00132371.
PR
XX (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
PA
XX Hu Y, Yao Y;
PI
XX WPI; 2002-751439/82.
DR N-PSDB; ABX14393.
XX
PT Tumor death induction ligand gene, gene expression protein and its
PT preparation method.
XX
PS Claim 7; Page 10 (disclosure); 17pp; Chinese.
XX
CC The present invention relates to the isolation of cDNA encoding human
CC tumour related apoptosis inducing ligand (Trail), and the Trail protein.
CC The Trail full length cDNA is cloned, and is utilised to create a Trail
CC prokaryotic expression system. The full length Trail cDNA is used to
CC respectively clone cDNA of soluble ectocytic segment Trail109 and Trail
CC 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic
CC expression systems. The prokaryotic expression systems created greatly
CC increase the expression and quantity of the Trail, Trail109, and Trail114
CC proteins, and may be useful in a new preparation for killing tumour
CC cells. The present sequence represents the partial human Trail protein,
CC Trail114
XX
SQ Sequence 168 AA;

Query Match 68.5%; Score 882; DB 5; Length 168;
Best Local Similarity 99.4%; Pred. No. 7.2e-78;
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 76 VRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE 135
Db 1 VRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE 60

Qy 136 LVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSK 195
Db 61 LVIHEKGFYIYSQTYFRFQEEIKENAKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSK 120

Qy 196 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 243
Db 121 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 168

RESULT 7
AAB08274
ID AAB08274 standard; protein; 166 AA.
XX
AC AAB08274;
XX
DT 04-DEC-2000 (first entry)
XX
DE Amino acid sequence of a human TNF ligand TRAIL.

XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
KW type II transmembrane protein; B cell stimulatory factor;
KW inflammatory disorder; immune disorder; rheumatoid arthritis;
KW lupus and graft versus host disease.
XX Homo sapiens.
OS
XX WO200047740-A2.
PN
XX 17-AUG-2000.
PD
XX 11-FEB-2000; 2000WO-US003653.
PF
XX 12-FEB-1999; 99US-0119906P.
PR 18-NOV-1999; 99US-0166271P.
XX (AMGE-) AMGEN INC.
PA
XX Boyle WJ, Hsu H;
PI
XX WPI; 2000-558217/51.
DR
XX Novel polypeptides comprising tumor necrosis factor ligand family
PT proteins, useful for treating inflammatory and immune disorders, e.g.
PT rheumatoid arthritis.
XX
PS Claim 14; Fig 9; 71pp; English.
XX
CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
CC specification describes an AGP-3 polypeptide, which is TNF ligand family
CC member. AGP-3 is a type II transmembrane protein, and is a potent B cell
CC stimulatory factor. Expression of AGP-3 correlates to increases in the
CC number of B cells and immunoglobulins produced. AGP-3 proteins,
CC antibodies, and nucleic acids may be used to treat inflammatory and
CC immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and
CC graft versus host disease. The nucleic acids may be used to regulate the
CC expression of an AGP-3 related protein. The AGP-3 proteins, antibodies
CC and nucleic acids are also useful for the detection of AGP-3 agonists,
CC antagonists and characterizing interactions with AGP-3 related proteins
XX
SQ Sequence 166 AA;

Query Match 68.2%; Score 878; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.7e-77;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 ERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 137
Db 1 ERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 60

Qy 138 IHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSKDA 197
Db 61 IHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSKDA 120

Qy 198 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 243
Db 121 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 166

RESULT 8
ABR84402
ID ABR84402 standard; protein; 167 AA.
XX
AC ABR84402;
XX
DT 09-OCT-2003 (first entry)
XX
DE TRAIL amino acid sequence.
XX
KW TRAIL; TNF-related apoptosis-inducing ligand; tumour; necrosin.
XX
OS Unidentified.


```

XX CN1380339-A.
XX
XX
PD 20-NOV-2002.
XX
XX
PF 10-APR-2001; 2001CN-00105946.
XX
PR 10-APR-2001; 2001CN-00105946.
XX
XX (CHEN-) CHENGDU DIAO PHARM GROUP CO LTD.
XX
XX Li B, Gao X, Liu Z;
XX
DR WPI; 2003-230973/23.
DR N-PSDB; ACC83357.
XX
PT Death induced ligand (TRAIL) cDNA and encoded polypeptide, useful for
PT inducing the death of tumor cells, is related to mutational human tumor
PT necrosin.
XX
XX Claim 4; Fig 2; 14pp; Chinese.
XX
CC The invention relates to a TNF-related apoptosis-inducing ligand encoding
CC (TRAIL) cDNA and its encoded polypeptide. The gene of the invention is
CC related to mutational human tumour necrosin. The polypeptide of the
CC invention is useful for inducing the death of tumour cells. The current
CC sequence represents the TRAIL amino acid sequence
XX
SQ Sequence 167 AA;

Query Match 67.3%; Score 866; DB 6; Length 167;
Best Local Similarity 98.2%; Pred. No. 2.6e-76;
Matches 166; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 75 LVREGRGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG 134
Db :|||||
1 MVRERG--RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG 58

QY 135 ELVHKEGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWS 194
Db |||||||
59 ELVHKEGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWS 118

QY 195 KDAEYGLYSIQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 243
Db |||||||
119 KDAEYGLYSIQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 167

RESULT 9
AAY71985
ID AAY71985 standard; protein; 161 AA.
XX
AC AAY71985;
XX
XX
DT 28-MAR-2001 (first entry)
XX
DE C-terminal region of human TRAIL protein.
XX
KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
KW Tumour necrosis factor and ApOL-related Leucocyte expressed Ligand 1;
KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
KW haemolytic anaemia; Grave's disease; myasthenia gravis; TRAIL protein;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 2..8
FT /label= Beta_strand
FT Region 32..34
FT /label= Beta_strand
```

```

FT Region 42..44
FT /label= Beta_strand
FT Region 47..50
FT /label= Beta_strand
FT Region 53..56
FT /label= Beta_strand
FT Region 61..72
FT /label= Beta_strand
FT Region 86..91
FT /label= Beta_strand
FT Region 99..109
FT /label= Beta_strand
FT Region 118..128
FT /label= Beta_strand
FT Region 133..143
FT /label= Beta_strand
FT Region 153..160
FT /label= Beta_strand
XX
PN WO200068378-A1.
XX
XX 16-NOV-2000.
PD
XX
XX 05-MAY-2000; 2000WO-US012266.
PF
XX
XX 06-MAY-1999; 99US-0132892P.
PR
PR 01-MAY-2000; 2000US-0201012P.
XX
XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
XX Shu HS;
PI
XX
XX WPI; 2001-016094/02.
DR
XX
PT Isolated TALL-1 protein is used to identify compounds that regulate B
PT lymphocyte proliferation, used to treat B lymphocyte associated
PT autoimmune disorders.
XX
PS Example 1; Fig 1b; 112pp; English.
XX
CC The present invention relates to Tumour necrosis factor (TNF) and ApOL-
CC related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
CC proteins (including homologues), and their antibodies. The invention in
CC particular relates to methods for regulating the interaction between TALL
CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.
CC TALL-1 protein is useful for identifying compounds that regulate B
CC lymphocyte proliferation. It is also useful for treating B lymphocyte
CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus
CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
CC corresponding nucleic acid sequence are also useful in diagnostic assays.
CC The present sequence is a C-terminal region of human TRAIL protein. which
CC has 20-25% sequence identity with the C-terminal region of human TALL-1
CC protein extracellular domain. TRAIL protein is a TNF family member
XX
SQ Sequence 161 AA;

Query Match 66.0%; Score 850; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 9.2e-75;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVHKEG 142
Db |||||||
1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVHKEG 60

QY 143 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 202
Db |||||||
61 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 120
```

Qy 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 10
ABR39855
ID ABR39855 standard; protein; 161 AA.
XX
AC ABR39855;
XX
XX 11-AUG-2003 (first entry)
DT
DE TNF family member, TRAIL (1d4v) protein fragment.
XX
KW RANK; receptor activator of necrosis factor k8; RANK ligand; RANKL;
KW tumour necrosis factor; TNF; TRAIL; cytokine.
XX
OS Unidentified.
XX
PN WO2003014077-A2.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-US025287.
XX
PR 09-AUG-2001; 2001US-0311163P.
PR 22-MAR-2002; 2002US-00105057.
XX
PA (BARN-) BARNES-JEWISH HOSPITAL.
XX
PI Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;
XX WPI; 2003-256526/25.
XX
XX Composition for identifying a compound with Receptor Activator of
PT Necrosis Factor k8, RANK modulating activity and for identifying RANK or
PT osteoprotegerin modulating compound, has a protein complex in crystalline
PT form.
XX
PS Disclosure; Fig 3; 66pp; English.
XX
XX The invention relates to a composition (I) comprising a protein complex
CC in crystalline form, where the complex comprises an amino acid sequence
CC of a Receptor Activator of Necrosis Factor k8 (RANK) Ligand (RANKL)
CC ectodomain. (I) is useful for identifying a compound with RANK modulating
CC activity, and for identifying a RANK or OPG modulating compound. (I) is
CC useful to intelligently design mutants that have altered biological
CC properties and for identifying and/or designing compounds that bind RANK
CC as an approach towards developing new therapeutic agents. (I) is also
CC useful to computationally screen small molecule databases for chemical
CC entities or compounds that can bind in whole, or in part, to RANK or
CC RANKL. The present sequence represents a tumour necrosis factor (TNF)
CC family member, TRAIL (1d4v), used in a structural-based alignment study
CC of murine RANKL protein
XX
SQ Sequence 161 AA;

Query Match 66.0%; Score 850; DB 6; Length 161;
Best Local Similarity 100.0%; Pred. No. 9.2e-75;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 142
Db 1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 60
Qy 143 FYYIYSQTYFRFQEEIKENTKNDQMVOYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 202
Db 61 FYYIYSQTYFRFQEEIKENTKNDQMVOYIYKYTSYPDPILLMKSARNCSWSKDAEYGLY 120

Qy 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
pb 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 11
ADC03335
ID ADC03335 standard; protein; 161 AA.
XX
AC ADC03335;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour necrosis factor family cytokine, TRAIL.
XX
KW RANKL ectodomain crystal complex; RANK; osteoprotegerin; OPG;
KW bone-forming compound; tumour necrosis factor; TNF family; cytokine;
KW TRAIL.
XX
OS Mus sp.
XX
PN US2003050223-A1.
XX
PD 13-MAR-2003.
XX
PF 09-AUG-2002; 2002US-00215446.
XX
PR 09-AUG-2001; 2001US-0311163P.
XX
PA (LAMJ/) LAM J.
PA (ROSS/) ROSS F P.
PA (TEIT/) TEITELBAUM S L.
PA (NELS/) NELSON C A.
PA (FREM/) FREMONT D H.
XX
PI Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;
XX WPI; 2003-605763/57.
XX
XX Composition comprising crystalline receptor activator of NfkappaB (RANK)
PT ligand ectodomain complex whose three-dimensional structural
PT representation is useful for identifying RANK or osteoprotegrin
PT modulating compound.
XX
PS Disclosure; Fig 3; 40pp; English.

The invention relates to a composition comprising a protein complex in crystalline form, where the complex comprises an amino acid sequence of a receptor activator of nuclear factor kappaB (NfkappaB) (RANK) ligand (RANKL) ectodomain. The three-dimensional structural representation of a RANKL ectodomain crystal complex, is useful for identifying a RANK or osteoprotegerin (OPG) modulating compound, and for identifying a compound with RANK modulating activity. The crystals permit the determination of the three-dimensional X-ray diffraction structure of the crystal-line polypeptide to high resolution. The atomic structure coordinates and structural information which comprises atomic structure coordinates are useful for identifying bone-forming compounds by methods which utilise the coordinates for solving the three-dimensional X-ray diffraction and/or solution structures of other proteins, including mutant forms, to high resolution. The structural information may also be used in a variety of molecular modeling and computer-based screening applications to, for example design mutants of the crystallized RANKL, its receptors, or a portion or fragment of RANKL or its receptors. The coordinates of RANKL crystal, or subsets of such structural coordinates of the RANKL crystal, are useful for designing or identifying candidate compounds capable of modulating RANK biological activity, and for identifying compounds which mimic the capability of RANKL to bind RANK molecules, thereby activating the receptor. The present sequence represents the amino acid sequence of the tumour necrosis factor family cytokine, TRAIL.

SQ Sequence 161 AA;

Query Match 66.0%; Score 850; DB 7; Length 161;
Best Local Similarity 100.0%; Pred. No. 9.2e-75;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 142
Db 1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 60
QY 143 FYIYISQTYFRFQEEIKENTKNDKQMVQVIKYKTSYPDPILLMKSARNSCWSKDAEYGLY 202
Db 61 FYIYISQTYFRFQEEIKENTKNDKQMVQVIKYKTSYPDPILLMKSARNSCWSKDAEYGLY 120
QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 12
AAU99301
ID AAU99301 standard; protein; 212 AA.
XX
AC AAU99301;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human TRAIL splice variant 8, rpl-6-6, protein.

XX Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
KW TRAIL; apoptosis; programmed cell death; differentiation; development;
KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
KW chromosome 3q26; rpl-6-6.
XX

OS Homo sapiens.

XX Key Location/Qualifiers
FH Domain 1. .16
FT /note= "Cytoplasmic domain"
FT Domain 17. .38
FT /note= "Transmembrane domain"
FT Domain 39. .212
FT /note= "Extracellular domain"
FT Misc-difference 209
FT /note= "Encoded by in-frame stop codon"

XX US2002061525-A1.

XX 23-MAY-2002.

XX 16-MAY-2001; 2001US-00855544.

XX 16-MAY-2000; 2000IL-00136156.

XX (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.

XX Yelin R, Khosravi R, Savitzky K;
PI WPI; 2002-479259/51.
XX

XX New splice variants of tumor necrosis factor-related apoptosis inducing
PT ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat
PT diseases or disorders associated with low expression of the variants.
XX

PS Claim 4; Fig 8; 29pp; English.

XX The invention discloses isolated, naturally occurring, polypeptide splice
CC variants of human tumour necrosis factor (TNF)-related apoptosis inducing
CC ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal
CC cellular differentiation and development of multicellular organisms.
CC Apoptosis is induced by certain cytokines which include TNF and TRAIL
CC (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane
CC protein which induces apoptosis and nuclear factor-B (NF-B) activation in
CC many tissues and cells. Receptors for TRAIL include two death domain

CC containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1
CC and DcR2, lacking the intracellular signalling death domain. TRAIL,
CC induced by type I interferons, induces apoptosis in tumour cells, whereas
CC normal cells are relatively resistant without showing significant toxic
CC side effects. Thus, TRAIL has the potential to be a very useful
CC antitumour agent. The naturally occurring splice variants may differ in
CC their cellular distribution, expression levels/timing and activity.
CC Determining these factors could provide possible mechanisms for the
CC induction of apoptosis of tumours cells. The splice variant polypeptides
CC and polynucleotides can be used in gene therapy, to raise antibodies, to
CC detect the levels, distribution and ratios of expression of TRAIL, and
CC its splice variants, in a biological sample and to identify compounds
CC which bind the variant TRAIL products and modulate its activity (agonists
CC and antagonists). Pharmaceutical compositions, comprising an expression
CC vector or any of the amino acid sequences, are useful for causing a
CC cytotoxic effect in cancer cells and for treatment of diseases which can
CC be ameliorated, cured or prevented by lowering or raising the level of
CC the amino acid sequences. The antibodies may also have a therapeutic
CC utility in blocking or decreasing the activity of the TRAIL variant
CC products. Diseases that may be treated include cancer, neurodegenerative
CC diseases, autoimmune diseases, diseases involved in the non-normal
CC development of tissues and aging. TRAIL's gene is located on chromosome
CC 3q26. The sequence presented is the human TNF-related apoptosis inducing
CC ligand (TRAIL) splice variant 8, rpl-6-6, protein which has had an C-
CC terminal section of the conserved TNF domain deleted
XX

SQ Sequence 212 AA;

Query Match 64.3%; Score 827; DB 5; Length 212;
Best Local Similarity 91.3%; Pred. No. 2.4e-72;
Matches 158; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE 60
Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIY 173
Db 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQKKKTSVSTCYFFQXNY 211

RESULT 13

ADI53053
ID ADI53053 standard; protein; 154 AA.
XX

AC ADI53053;

XX 22-APR-2004 (first entry)

DE Human TRAIL protein (aa 119-281).

XX protein co-ordinate data; cytostatic; antiallergic; immunosuppressive;
KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;
KW antidiabetic; dermatological; antiasthmatic; neutrokin-alpha;
KW crystallography; cancer; allergic disorder; autoimmune disease;
KW rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;
KW systemic lupus erythematosus; asthma.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1. .154
FT /note= "X shown in the sequence are illegible in the
FT figure sequence"

XX WO2003050134-A2.

XX 19-JUN-2003.

XX

PF 07-NOV-2002; 2002WO-US035661.
XX
PR 07-NOV-2001; 2001US-0331049P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Li Y, Oren DE, Arnold E, Volovik Y;
XX
DR WPI; 2003-532895/50.
XX
PT New crystalline Neutrokine-alpha protein, useful for designing compounds
PT that bind, inhibit or mimic a Neutrokine-alpha protein or enhance the
PT activity of a Neutrokine-alpha protein for treating e.g. cancer or
PT allergic disorders.
XX
PS Disclosure; Fig 1; 362pp; English.
XX
CC The invention relates to a neutrokine-alpha protein in crystalline form.
CC The crystalline neutrokine-alpha protein is useful for designing
CC molecules that have biological activity or compounds that bind, inhibit
CC or mimic a neutrokine-alpha protein and/or enhance the activity of a
CC neutrokine-alpha protein. The three-dimensional structure of a neutrokine
CC -alpha protein is useful in determining the three-dimensional of other
CC neutrokine-alpha proteins and their homologs. The compounds that mimic,
CC prevent or inhibit the activity of the protein are useful for treating
CC cancer, allergic disorders, or autoimmune diseases such as rheumatoid
CC arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus
CC erythematosus or asthma. This sequence represents the human TRAIL protein
CC amino acids 119-281 which is used in the invention for comparison to the
CC human neutrokine-alpha protein (ADI53050).
XX
SQ Sequence 154 AA;

Query Match 59.4%; Score 764.5; DB 7; Length 154;
Best Local Similarity 90.8%; Pred. No. 2e-66;
Matches 148; Conservative 0; Mismatches 6; Indels 9; Gaps 1;

Qy 81 PQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE 140
Db 1 PQVAAHITGXGRG-----KNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE 51

Qy 141 KGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSKDAEYG 200
Db 52 KGFYIYSQTYFRFQEEIKENTKNQKQMVQYIYKYTXXXXPILLMKSARNSCWSKDAEYG 111

Qy 201 LYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 112 LYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 154

RESULT 14
ADO24774
ID ADO24774 standard; protein; 171 AA.
XX
AC ADO24774;
XX
DT 29-JUL-2004 (first entry)
XX
DE Cat soluble TRAIL protein.
XX
KW cytotostatic; dermatological; antirheumatic; antiarthritic;
KW neuroprotective; canine; feline; TNF-related apoptosis-inducing ligand;
KW TRAIL; apoptosis; cancer; neurodegenerative disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; diagnosis; genetic testing;
KW angiogenesis.
XX
OS Felis catus.
XX
PN WO2004039307-A2.
XX
PD 13-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-IB004635.

XX 30-OCT-2002; 2002US-0422342P.
PR (PFIZ) PFIZER PROD INC.
PA
XX Cai JH, Rong S;
PI
XX WPI; 2004-376043/35.
DR N-PSDB; ADO24773.
XX
PT Novel isolated canine or feline TNF-related apoptosis-inducing ligand
PT polypeptide, useful for diagnostic evaluation, genetic testing and/or
PT prognosis of angiogenesis-related disorders, such as cancer.
XX
PS Disclosure; SEQ ID NO 29; 151pp; English.
XX
CC The invention relates to an isolated polypeptide (I) comprising a canine
CC or feline TNF-related apoptosis-inducing ligand (TRAIL) sequence and
CC optionally a fusion peptide fused to the polypeptide. Modulators of (I)
CC are useful for treating an apoptosis-related disorder in a subject. The
CC apoptosis-related disorder is chosen from cancer, neurodegenerative
CC disease, lupus erythematosus, rheumatoid arthritis and multiple
CC sclerosis. (I) is useful for diagnostic evaluation, genetic testing
CC and/or prognosis of angiogenesis-related disorders, such as cancer. This
CC sequence represents a gene encoding a cat soluble TRAIL protein used in
CC the invention.
XX
SQ Sequence 171 AA;

Query Match 59.4%; Score 764; DB 8; Length 171;
Best Local Similarity 84.2%; Pred. No. 2.6e-66;
Matches 144; Conservative 13; Mismatches 12; Indels 2; Gaps 1;

Qy 75 LVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG 134
Db 1 MVRERGPQVAAHITGTRRRSTFPVPSSKNEKALGQKINSWESSRKGHSFLNHLRNG 60

Qy 135 ELVTHEKGFYIYSQTYFRFQ--EEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSC 192
Db 61 ELVTHQRGFYIYSQTYFRFQPEETEQRNKRKNQMVQYIYKYTSYDPDILLMKSARNSC 120

Qy 193 WSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 WSKDSEYGLYSIQGGIFELKENDRIFVSVSNEQLIDMDQEAFFGAFLIG 171

RESULT 15
ADO24776
ID ADO24776 standard; protein; 201 AA.
XX
AC ADO24776;
XX
DT 29-JUL-2004 (first entry)
XX
DE Cat soluble TRAIL with a C-terminal V5-His tag protein.
XX
KW cytotostatic; dermatological; antirheumatic; antiarthritic;
KW neuroprotective; canine; feline; TNF-related apoptosis-inducing ligand;
KW TRAIL; apoptosis; cancer; neurodegenerative disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; diagnosis; genetic testing;
KW angiogenesis.
XX
OS Felis catus.
XX
PN WO2004039307-A2.
XX
PD 13-MAY-2004.
XX
PF 21-OCT-2003; 2003WO-IB004635.
XX
PR 30-OCT-2002; 2002US-0422342P.
XX
PA (PFIZ) PFIZER PROD INC.

XX Cai JH, Rong S;
PI
XX
DR WPI; 2004-376043/35.
DR N-PSDB; ADO24775.
XX
PT Novel isolated canine or feline TNF-related apoptosis-inducing ligand
PT polypeptide, useful for diagnostic evaluation, genetic testing and/or
PT prognosis of angiogenesis-related disorders, such as cancer.
XX
PS Disclosure; SEQ ID NO 31; 151pp; English.
XX
CC The invention relates to an isolated polypeptide (I) comprising a canine
CC or feline TNF-related apoptosis-inducing ligand (TRAIL) sequence and
CC optionally a fusion peptide fused to the polypeptide. Modulators of (I)
CC are useful for treating an apoptosis-related disorder in a subject. The
CC apoptosis-related disorder is chosen from cancer, neurodegenerative
CC disease, lupus erythematosus, rheumatoid arthritis and multiple
CC sclerosis. (I) is useful for diagnostic evaluation, genetic testing
CC and/or prognosis of angiogenesis-related disorders, such as cancer. This
CC sequence represents a gene encoding a cat TRAIL protein with a V5-His Tag
CC at the C-terminus and used in the invention.
XX
SQ Sequence 201 AA;

Query Match 59.4%; Score 764; DB 8; Length 201;
Best Local Similarity 84.2%; Pred. No. 3.3e-66;
Matches 144; Conservative 13; Mismatches 12; Indels 2; Gaps 1;

Qy 75 LVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRGHSFSLNHLRNG 134
Db :|||||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:
1 MVRERGPORVAAHITGTSRRRSTFPVPSSKNEKALGQKINSWESSRKHSFSLNHLRNG 60

Qy 135 ELVIHEKGFYIYSQTYFRFQ--EEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSC 192
Db |||||:|||||:|||||:|:|:|:|:|||||:|||||:|||||:|||||:
61 ELVIHQRFYIYSQTYFRFQEPETEQRNKNQMVQYIYKYTSYDPDPILLMKSARNSC 120

Qy 193 WSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG 243
Db ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 WSKDSEYGLYSIQGGIFELKENDRIFVSVSNEQLIDMDQEAASFGAFLIG 171

Search completed: June 3, 2005, 06:40:57
Job time : 164 secs

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Result No.	Score	Query Match %	Length	DB	ID	Description
1	892.5	69.3	228	17	US-10-855-559-4	Sequence 4, Appli
2	887	68.9	168	9	US-09-900-530A-10	Sequence 10, Appl
3	887	68.9	168	17	US-10-981-989-14	Sequence 14, Appl
4	878	68.2	166	9	US-09-779-050A-16	Sequence 16, Appl
5	859	66.7	164	13	US-10-116-378-29	Sequence 29, Appl
6	859	66.7	164	17	US-10-959-537-29	Sequence 29, Appl
7	850	66.0	161	14	US-10-216-074-7	Sequence 7, Appli
8	849	66.0	161	14	US-10-338-083-11	Sequence 11, Appl
9	849	66.0	161	16	US-10-611-399-11	Sequence 11, Appl
10	849	66.0	161	17	US-10-794-751-11	Sequence 11, Appl
11	835	64.9	158	17	US-10-778-890-10	Sequence 10, Appl
12	826	64.2	208	9	US-09-855-544A-16	Sequence 16, Appl
13	746.5	58.0	188	9	US-09-855-544A-14	Sequence 14, Appl


```
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 29
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-29

Query Match          66.7%; Score 859; DB 13; Length 164;
Best Local Similarity 99.4%; Pred. No. 1.9e-71;
Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 80 GQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIH 139
    |||||||
Db 1 GQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIH 60

QY 140 EKGYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEY 199
    |||||||
Db 61 EKGYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEY 120

QY 200 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
    |||||||
Db 121 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 164

RESULT 6
US-10-959-537-29
; Sequence 29, Application US/10959537
; Publication No. US20050069983A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/959,537
; CURRENT FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US/09/247,225
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 29
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-537-29

Query Match          66.7%; Score 859; DB 17; Length 164;
Best Local Similarity 99.4%; Pred. No. 1.9e-71;
Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 80 GQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIH 139
    |||||||
Db 1 GQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIH 60

QY 140 EKGYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEY 199
    |||||||
Db 61 EKGYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEY 120

QY 200 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
    |||||||
Db 121 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 164

RESULT 7
US-10-216-074-7
; Sequence 7, Application US/10216074
; Publication No. US20030148445A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-7

Query Match          66.0%; Score 850; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.3e-70;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 142
    |||||||
Db 1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 60

QY 143 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 202
    |||||||
Db 61 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 120

QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
    |||||||
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 161

RESULT 8
US-10-338-083-11
; Sequence 11, Application US/10338083
; Publication No. US20030166559A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-11

Query Match          66.0%; Score 849; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.6e-70;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 QORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEK 141
    |||||||
Db 1 QORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEK 60

QY 142 GFYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGL 201
    |||||||
Db 61 GFYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGL 120
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Qy 202 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
|
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 161

RESULT 9
US-10-611-399-11
; Sequence 11, Application US/10611399
; Publication No. US20040170602A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
; FILE REFERENCE: A-71273-3
; CURRENT APPLICATION NUMBER: US/10/611,399
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-611-399-11

Query Match 66.0%; Score 849; DB 16; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.6e-70;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV1HEK 141
|
Db 1 QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV1HEK 60

Qy 142 GFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGL 201
|
Db 61 GFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGL 120

Qy 202 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
|
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 161

RESULT 10
US-10-794-751-11
; Sequence 11, Application US/10794751
; Publication No. US20050048626A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Thomson, Adam Read
; APPLICANT: Zhukovsky, Eugene Alexander
; TITLE OF INVENTION: BAFF VARIANTS AND METHODS THEREOF
; FILE REFERENCE: A-72175-1
; CURRENT APPLICATION NUMBER: US/10/794,751
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/452,707
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/482,081
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 60/523,880
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US 60/528,104
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-751-11

Query Match 66.0%; Score 849; DB 17; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.6e-70;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 82 QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV1HEK 141
|
Db 1 QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV1HEK 60

Qy 142 GFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGL 201
|
Db 61 GFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGL 120

Qy 202 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
|
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 161

RESULT 11
US-10-778-890-10
; Sequence 10, Application US/10778890
; Publication No. US20050112596A1
; GENERAL INFORMATION:
; APPLICANT: TSCHOPP, JURG
; TITLE OF INVENTION: APRIL-A NOVEL PROTEIN WITH GROWTH EFFECTS
; FILE REFERENCE: A049 US
; CURRENT APPLICATION NUMBER: US/10/778,890
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: US/09/520,489
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/19191
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/079,384
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/058,786
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-778-890-10

Query Match 64.9%; Score 835; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 3.1e-69;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 85 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV1HEKGFY 144
|
Db 1 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV1HEKGFY 60

Qy 145 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSI 204
|
Db 61 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSI 120

Qy 205 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
|
Db 121 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 158

RESULT 12
US-09-855-544A-16
; Sequence 16, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS

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; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-16

Query Match          64.2%; Score 826; DB 9; Length 208;
Best Local Similarity 96.3%; Pred. No. 3e-68;
Matches 156; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQVRKMILRTSEE 60
Db 39 TNELKQMDKYSGKIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQVRKMILRTSEE 98

Qy 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENT 162
Db 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQKGGKTS 200

RESULT 13
US-09-855-544A-14
; Sequence 14, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-14

Query Match          58.0%; Score 746.5; DB 9; Length 188;
Best Local Similarity 61.7%; Pred. No. 6.1e-61;
Matches 150; Conservative 0; Mismatches 0; Indels 93; Gaps 1;

Qy 1 TNELKQMDKYSGKIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQVRKMILRTSEE 60
Db 39 TNELKQMDKYSGKIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQVRKMILRTSEE 98

Qy 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQ----- 104

Qy 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD 180
Db 105 -----ENTKNDKQMVQYIYKYTSYPD 125

Qy 181 PILLMKSARNSCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 126 PILLMKSARNSCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 185

Qy 241 LVG 243
Db 186 LVG 188

RESULT 14
US-09-779-050A-17
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; Sequence 17, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-17

Query Match          49.4%; Score 636; DB 9; Length 172;
Best Local Similarity 71.4%; Pred. No. 9.3e-51;
Matches 120; Conservative 20; Mismatches 22; Indels 6; Gaps 1;

Qy 81 PQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 140
Db 4 PQVAAHITGTRRSNSALIPISKDGKTGQKIESWESSRKGHSFLNHLVFRNGELV 63

Qy 141 KGFYIYSQTYFRFQEE-----IKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWS 194
Db 64 EGLYIYSQTYFRFQEAEDASKMVSXDKVTKQLVQYIYKYTSYDPDIVLMKSARNSCWS 123

Qy 195 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLV 242
Db 124 RDAEYGLYSIQGGIFELKKNDRIFVSVTNEHLMDLDQEAFFGAPLI 171

RESULT 15
US-10-286-696-12
; Sequence 12, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. US20030129706A1e1 Member of the TNF Ligand Supergene Fa
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-696-12

Query Match          34.7%; Score 446; DB 14; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 ERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 137
Db 1 ERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 60

Qy 138 IHEKGFYIYSQTYFRFQEEIKENT 162
Db 61 IHEKGFYIYSQTYFRFQEEIKENT 85

Search completed: June 3, 2005, 06:57:06
Job time : 141 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 06:38:16 ; Search time 42 Seconds
(without alignments)
431.898 Million cell updates/sec

Title: US-10-662-431-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNELKQMQRKYSKSGIACFL.....NEHLIDMDHEASFFGAFVLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 410927

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	930	72.3	177	3	US-09-105-343A-7
2	850	66.0	161	4	US-09-565-423-7
3	654	50.8	183	3	US-09-105-343A-8
4	544	42.3	169	4	US-09-569-611C-29
5	446	34.7	85	4	US-09-632-287A-12
6	425	33.0	121	4	US-09-513-999C-7833
7	292	22.7	120	4	US-09-569-611C-32
8	291	22.6	101	1	US-08-670-354-4
9	291	22.6	101	3	US-09-320-424-4
10	291	22.6	101	4	US-09-825-563-4
11	291	22.6	101	5	PCT-US96-10895-4
12	291	22.6	122	4	US-09-569-611C-31
13	245.5	19.1	87	4	US-09-632-287A-13
14	228.5	17.8	173	4	US-09-396-937-10
15	228.5	17.8	173	4	US-09-396-937-12
16	228.5	17.8	187	4	US-09-396-937-8
17	210	16.3	182	4	US-09-396-937-16
18	208	16.2	188	4	US-09-396-937-14
19	202.5	15.7	173	4	US-09-396-937-20
20	195.5	15.2	173	4	US-09-396-937-18
21	189.5	14.7	179	3	US-08-339-214-22
22	182.5	14.2	186	4	US-09-254-180C-175
23	182	14.1	138	3	US-08-339-214-20
24	181.5	14.1	178	3	US-08-339-214-84
25	181.5	14.1	179	3	US-08-649-100-9
26	181.5	14.1	179	3	US-08-339-214-6
27	181.5	14.1	179	4	US-09-254-180C-176

28	179	13.9	137	3	US-08-339-214-18	Sequence 18, Appl
29	178	13.8	145	3	US-08-630-172-5	Sequence 5, Appli
30	178	13.8	145	3	US-09-375-419-5	Sequence 5, Appli
31	177.5	13.8	179	3	US-08-339-214-14	Sequence 14, Appl
32	175.5	13.6	149	3	US-08-584-031-17	Sequence 17, Appl
33	175.5	13.6	149	4	US-09-934-465-17	Sequence 17, Appl
34	175	13.6	148	4	US-09-582-450-17	Sequence 17, Appl
35	175	13.6	152	4	US-09-496-118B-8	Sequence 8, Appli
36	173	13.4	138	3	US-08-339-214-4	Sequence 4, Appli
37	173	13.4	138	3	US-08-339-214-12	Sequence 12, Appl
38	173	13.4	138	3	US-08-339-214-81	Sequence 81, Appl
39	173	13.4	138	4	US-09-565-423-5	Sequence 5, Appli
40	173	13.4	138	4	US-09-254-180C-177	Sequence 177, App
41	173	13.4	139	3	US-08-339-214-80	Sequence 80, Appl
42	173	13.4	139	4	US-08-968-686-4	Sequence 4, Appli
43	173	13.4	141	3	US-09-286-529-22	Sequence 22, Appl
44	173	13.4	141	3	US-08-339-214-79	Sequence 79, Appl
45	170	13.2	136	3	US-08-339-214-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-09-105-343A-7
; Sequence 7, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-7

Query Match 72.3%; Score 930; DB 3; Length 177;
Best Local Similarity 99.4%; Pred. No. 1.6e-88;
Matches 176; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 67 EKQONISPLVRRGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126

Db 1 EKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 60
QY 127 SNLHLRNGELVIHEKGFYIYSQTYFRFOBEIKENTKNDKQMVQYIYKYTSYDPDPILLMK 186
Db 61 SNLHLRNGELVIHEKGFYIYSQTYFRFOBEIKENTKNDKQMVQYIYKYTSYDPDPILLMK 120
QY 187 SARNSCWSDAEBGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 SARNSCWSDAEBGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 177

RESULT 2
US-09-565-423-7
; Sequence 7, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-7

Query Match 66.0%; Score 850; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.9e-80;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 142
Db 1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 60
QY 143 FYYIYSQTYFRFOBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 202
Db 61 FYYIYSQTYFRFOBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 120
QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 3
US-09-105-343A-8
; Sequence 8, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-8

Query Match 50.8%; Score 654; DB 3; Length 183;
Best Local Similarity 68.7%; Pred. No. 7.6e-60;
Matches 125; Conservative 22; Mismatches 29; Indels 6; Gaps 1;
QY 67 EKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126
Db 1 EKQLSTPPLPRGGRPOKVAAHITGITRRNSALIPISKDGTGKIESWESSRKGHSFL 60
QY 127 SNLHLRNGELVIHEKGFYIYSQTYFRFOEE-----IKENTKNDKQMVQYIYKYTSYDP 180
Db 61 NHVLFNGELVIEQEGLYIYSQTYFRFOEAEDASKMYSKDKVRTKQLVQYIYKYTSYDP 120
QY 181 PILLMKSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 121 PIVLMKSARNSCWSDAEYGLYSIQGGLFELKKNDRIFVSVTNEHLMDLDQEAFFGAF 180
QY 241 LV 242
Db 181 II 182

RESULT 4
US-09-569-611C-29
; Sequence 29, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-29

Query Match 42.3%; Score 544; DB 4; Length 169;
Best Local Similarity 99.0%; Pred. No. 1.8e-48;
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMQDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEE 60
Db 63 TNELKQMQDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEE 122
QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSK 104

Db 123 TISTVQEKQONISPLVRGQPVAAAHITGTRGRSNTLSSPNSR 166

RESULT 5

US-09-632-287A-12

; Sequence 12, Application US/09632287A

; Patent No. 6521422

; GENERAL INFORMATION:

; APPLICANT: Hsu, Hailing

; APPLICANT: Wooden, Scott K

; APPLICANT: Boyle, William J

; TITLE OF INVENTION: Fhm, A No. 6521422e1 Member of the TNF Ligand Supergene Family

; FILE REFERENCE: 01017/35550A

; CURRENT APPLICATION NUMBER: US/09/632,287A

; CURRENT FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: US 60/147,294

; PRIOR FILING DATE: 1999-08-04

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12

; LENGTH: 85

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-632-287A-12

Query Match 34.7%; Score 446; DB 4; Length 85;

Best Local Similarity 100.0%; Pred. No. 9.6e-39;

Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 ERGPQVAAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHLRNGELV 137

Db 1 ERGPQVAAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHLRNGELV 60

QY 138 IHEKGFYIYSQTYFRFQEEIKENT 162

Db 61 IHEKGFYIYSQTYFRFQEEIKENT 85

RESULT 6

US-09-513-999C-7833

; Sequence 7833, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 7833

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: -32..-1

; OTHER INFORMATION: score 5.3

; OTHER INFORMATION: seq VIFTVLLQSLCVA/VT

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: -18

; OTHER INFORMATION: Xaa=Asn or Thr

US-09-513-999C-7833

Query Match 33.0%; Score 425; DB 4; Length 121;

Best Local Similarity 100.0%; Pred. No. 2.4e-36;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILTSEE 60

Db 39 TNELKQMDKYSGKIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILTSEE 98

QY 61 TISTVQEKQONISPLVRERG 80

Db 99 TISTVQEKQONISPLVRERG 118

RESULT 7

US-09-569-611C-32

; Sequence 32, Application US/09569611C

; Patent No. 6720182

; GENERAL INFORMATION:

; APPLICANT: SAVITZKY et al.

; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS

; FILE REFERENCE: 2786-0151P

; CURRENT APPLICATION NUMBER: US/09/569,611C

; CURRENT FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 32

; LENGTH: 120

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-569-611C-32

Query Match 22.7%; Score 292; DB 4; Length 120;

Best Local Similarity 98.1%; Pred. No. 1.5e-22;

Matches 52; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKM 53

Db 63 TNELKQMDKYSGKIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKV 115

RESULT 8

US-08-670-354-4

; Sequence 4, Application US/08670354

; Patent No. 5763223

; GENERAL INFORMATION:

; APPLICANT: Steven R. Wiley and

; APPLICANT: Raymond G. Goodwin.

; TITLE OF INVENTION: Cytokine That Induces Apoptosis

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple 7.5.2

; SOFTWARE: Microsoft Word, Version 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/670,354

; FILING DATE: 25-JUN-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/496,632

; FILING DATE: 29-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/548,368

; FILING DATE: 01-NOV-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Anderson, Kathryn A.

; REGISTRATION NUMBER: 32,172

```
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-670-354-4

Query Match      22.6%; Score 291; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 52
Db 39 TNELKQMDDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

RESULT 9
US-09-320-424-4
; Sequence 4, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
; US-09-320-424-4

Query Match      22.6%; Score 291; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 52
Db 39 TNELKQMDDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

RESULT 10
US-09-825-563-4
; Sequence 4, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
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; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
; US-09-825-563-4

Query Match      22.6%; Score 291; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 52
Db 39 TNELKQMDDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

RESULT 11
PCT-US96-10895-4
; Sequence 4, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10895-4
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RESULT 14

Qy	146	IYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYDPILLMKSARNSCWSKDAEYGLYSI	204
Db	72	LYANISFRHHETSGSVPTDYQLMVYVVVKTSIKIPSSHNLKGGSTKNWMSGNSEFHFYSI	131
Qy	205	YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV	242
Db	132	NVGGFYKLRAGEEISIQVSNPSLLDPDQDATYFGAFV	169

Search completed: June 3, 2005, 06:53:39
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 06:16:49 ; Search time 43 Seconds
(without alignments)
487.823 Million cell updates/sec

Title: US-10-662-431-2
Perfect score: 1478
Sequence: 1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1478	100.0	281	1	US-08-670-354-2 Sequence 2, Appli
2	1478	100.0	281	3	US-08-584-031-1 Sequence 1, Appli
3	1478	100.0	281	3	US-08-780-496-1 Sequence 1, Appli
4	1478	100.0	281	3	US-08-883-086-10 Sequence 10, Appl
5	1478	100.0	281	3	US-09-320-424-2 Sequence 2, Appli
6	1478	100.0	281	3	US-09-333-593A-6 Sequence 6, Appli
7	1478	100.0	281	4	US-09-157-864-11 Sequence 11, Appl
8	1478	100.0	281	4	US-09-825-563-24 Sequence 2, Appli
9	1478	100.0	281	4	US-09-919-039-118 Sequence 118, App
10	1478	100.0	281	4	US-09-582-450-1 Sequence 1, Appli
11	1478	100.0	281	4	US-09-934-465-1 Sequence 1, Appli
12	1478	100.0	281	4	US-10-011-125A-4 Sequence 4, Appli
13	1478	100.0	281	5	PCT-US96-10895-2 Sequence 2, Appli
14	1469	99.4	279	3	US-09-072-993C-3 Sequence 3, Appli
15	1238	83.8	271	4	US-09-569-611C-30 Sequence 30, Appl
16	988	66.8	253	3	US-09-320-424-11 Sequence 11, Appl
17	988	66.8	253	4	US-09-825-563-11 Sequence 13, Appl
18	988	66.8	256	3	US-09-320-424-13 Sequence 13, Appl
19	988	66.8	256	4	US-09-825-563-13 Sequence 7, Appli
20	930	62.9	177	3	US-09-105-343A-7 Sequence 6, Appli
21	930	62.9	291	1	US-08-670-354-6 Sequence 6, Appli
22	930	62.9	291	3	US-09-320-424-6 Sequence 6, Appli
23	930	62.9	291	4	US-09-825-563-6 Sequence 6, Appli
24	930	62.9	291	5	PCT-US96-10895-6 Sequence 6, Appli
25	850	57.5	161	4	US-09-565-423-7 Sequence 7, Appli
26	735	49.7	169	4	US-09-569-611C-29 Sequence 29, Appl
27	654	44.2	183	3	US-09-105-343A-8 Sequence 8, Appli

28	611	41.3	121	4	US-09-513-999C-7833	Sequence 7833, Ap
29	483	32.7	120	4	US-09-569-611C-32	Sequence 32, Appl
30	482	32.6	101	1	US-08-670-354-4	Sequence 4, Appli
31	482	32.6	101	3	US-09-320-424-4	Sequence 4, Appli
32	482	32.6	101	4	US-09-825-563-4	Sequence 4, Appli
33	482	32.6	101	5	PCT-US96-10895-4	Sequence 4, Appli
34	482	32.6	122	4	US-09-569-611C-31	Sequence 31, Appl
35	446	30.2	85	4	US-09-632-287A-12	Sequence 12, Appl
36	258.5	17.5	294	3	US-08-996-139-11	Sequence 11, Appl
37	258.5	17.5	294	3	US-08-995-659-11	Sequence 11, Appl
38	258.5	17.5	294	3	US-09-215-649A-11	Sequence 11, Appl
39	258.5	17.5	294	4	US-09-577-780-11	Sequence 11, Appl
40	258.5	17.5	294	4	US-09-577-800-11	Sequence 11, Appl
41	258.5	17.5	294	4	US-09-466-496-11	Sequence 11, Appl
42	258.5	17.5	294	4	US-09-871-856-11	Sequence 11, Appl
43	258.5	17.5	294	4	US-09-871-291-11	Sequence 11, Appl
44	258.5	17.5	294	4	US-09-877-650-11	Sequence 11, Appl
45	258.5	17.5	294	4	US-09-865-363-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

Query Match 100.0%; Score 1478; DB 1; Length 281;

Qy 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7
US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-157-864-11

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGQ 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8
US-09-825-563-2
; Sequence 2, Application US/098255563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-09-825-563-2

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 9
US-09-919-039-118
; Sequence 118, Application US/09919039

; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
US-09-919-039-118

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWKSDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 10
US-09-582-450-1
; Sequence 1, Application US/09582450
; Patent No. 6740739
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Kelley, Robert F.
; APPLICANT: O'Connell, Mark P.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Schwall, Ralph H.
; TITLE OF INVENTION: Apo-2 Ligand
; FILE REFERENCE: P0978P4
; CURRENT APPLICATION NUMBER: US/09/582,450
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/007,886
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 09/060,533
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-450-1

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWKSDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 11
US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. 6746668
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNCSWKSDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 12
US-10-011-125A-4
; Sequence 4, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching


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; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011.125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125A-4

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
      |||
Db      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60

QY      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPO 120
      |||
Db      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPO 120

QY      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
      |||
Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY      181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
      |||
Db      181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 13
PCT-US96-10895-2
; Sequence 2, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match      100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60
      |||
Db      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKE 60

QY      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPO 120
      |||
Db      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPO 120

QY      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
      |||
Db      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY      181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
      |||
Db      181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 14
US-09-072-993C-3
; Sequence 3, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-3
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Query Match      99.4%; Score 1469; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 3.1e-148;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKEDD 62
      |||
Db      1 MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYYVFTNELKQMDKYSKSGIACFLKEDD 60

QY      63 SYWDPNDEESMNSPCWQVKWQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGPO 122
      |||
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Db 61 SYWDPNDESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPQV 120
QY 123 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY 182
Db 121 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY 180
QY 183 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSI 242
Db 181 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSI 240
QY 243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279

RESULT 15
US-09-569-611C-30
; Sequence 30, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-30

Query Match 83.8%; Score 1238; DB 4; Length 271;
Best Local Similarity 85.4%; Pred. No. 1.3e-123;
Matches 240; Conservative 2; Mismatches 5; Indels 34; Gaps 2;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 25 MAMMEVQGGPSLGQTCVLIVIFTVLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 84

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
Db 85 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK-----KSNKIFLPLVRERGPQ 130

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 131 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 190

QY 181 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
Db 191 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 250

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 251 SIYQG-----IDMDHEASFFGAFLVG 271

Search completed: June 3, 2005, 06:26:29
Job time : 45 secs

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